Symposium on Human Impacts on Marine Functional Connectivity

Book of abstracts

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Theme session 1 – Pervasive human impacts on the environment and trends in marine connectivity

22 May 2023

Conveners:
Audrey Darnaude, French National Centre for Scientific Research
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Humans have depended on and impacted marine ecosystems for thousands of years. From fishing and aquaculture to habitat destruction, pollution, climate change, and the expansion of offshore renewable energy and mining or fossil fuel extraction, impacts have diversified, often becoming chronic, modifying benthic and pelagic seascapes and ultimately impacting marine connectivity. Moreover, human activities have directly resulted in the forced, intentional and unintentional connection of marine populations, and the transport of non-indigenous species into new areas.

This session calls for studies on temporal changes in marine connectivity patterns associated with human impacts, and their consequences on resource or ecosystem resilience.

S1 Keynote: Human impacts on coastal ecosystems through scales: implications for management and adaptations

Keynote: Stephanie D’Agata
French National Centre for Scientific Research

Abstract

Accelerating social and environmental changes have led to the degradation of coastal ecosystems and the associated decline in biodiversity and multifunctionality (i.e., the full range of simultaneous ecosystem functions), altering the productivity and stability of associated ecosystem services and benefits to people who depend on them. Ensuring a sustainable future for coastal ecosystems and the provision of ecosystem services requires managing coastal ecosystems as social-ecological systems, characterized by multi-scale interactions, dependencies, and feedbacks between socio-economic and ecological systems. To improve our understanding of the sustainability of coastal social-ecological systems, it is imperative to address uncertainties and knowledge gaps in the socio-economic and ecological determinants of coastal ecosystem functioning and associated ecosystem services across scales. This presentation will explore, using examples mainly from coral reefs ecosystems, the interactions between human and ecological systems across scales, and examine the role of marine protected areas in sustaining ecosystem services now and in the future. It will also discuss the importance of interdisciplinary research in advancing our understanding of the dynamic of coastal socio-ecological systems.

S1O1 Short and long-term temperature variations drive recruitment and connectivity in marine and estuarine juvenile fishes.

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Abstract

Understanding how climatic conditions affect key species in the long term is critical for fisheries management as well as for species and ecosystem conservation. We aimed to analyse the variability of recruitment and connectivity of *Dicentrarchus labrax*, *Platichthys flesus*, *Solea solea*, *Pomatoschistus microps* and *Pomatoschistus minutus* in the Mondego estuary (Portugal) and to relate this variability to the dominant environmental factors within the estuary and in the adjacent coastal zone, during a period of 17 years (2003 - 2019). A dynamic factor analysis (DFA) showed three common trends in the data, associated with different habitat use patterns and life cycles of the five species (marine juvenile migrants vs estuarine residents). The best model included three common trends plus estuary water temperature and the Atlantic Multidecadal Oscillation (AMO) index lagged by 1 year as explanatory variables, reinforcing the thermophilic nature of recruitment in both marine juvenile migrants and estuarine resident fishes. Individual correlations also showed a similar relationship between these species and water temperature-related variables, responding positively to a slight increase in water temperature. However, a wide-ranging change in the AMO contributed to a regime shift in the North Atlantic in 2010, which coincided with a shift in the common trends between 2010 and 2012, namely a marked decrease in *P. flesus* and *S. solea* trend. This work demonstrates the thermophilic nature of fish recruitment and connectivity between early ontogenic habitats, and the need to observe key biological processes to develop better conservation and management strategies, particularly in the context of species responses to climate change.

S1O2 Global warming may reinstate connectivity between the Mediterranean Sea and tropical West Africa.

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Abstract

Global climate change is affecting marine life in complex and accelerating ways. Changes in the distributional range of marine species are already among the most prominent effects, leading to major biotic reorganizations and novel connections between historically isolated biota. These processes, however, are only now becoming evident. Looking back into Earth´s history enables the understanding of how communities responded to past warming events. In the context of future climate change the Last Interglacial (LIG) period is particularly relevant as it represents the most recent time with temperatures in the range of those predicted in future climate scenarios. The Mediterranean Sea is warming at a rate higher than the global average and thus a priority area for the study of its consequences. During the LIG, the Mediterranean marine biota was enriched by the so-called "Senegalese guests", that is, tropical West African species that expanded their range into the basin as a response to warming but then regressed to the tropical belt during the cooling that followed the Last Interglacial. Based on this palaeoecological evidence, we explore future climate scenarios to test the hypothesis that connectivity between the Mediterranean Sea and tropical West Africa could be reinstated. We use the LIG fossil record and modern occurrences of nine molluscan "Senegalese guests" to build a multi-temporal envelope of climate and species data and to project their distributions in future climate scenarios. Our results suggest that the Mediterranean basin will become progressively suitable for tropical West African species and that increased connectivity along the north-western African coast will enable their arrival.

S1O3 Assessment of synchrony in temporal changes in biodiversity of fish communities in connected marine and estuarine ecosystems

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Abstract

Aquatic ecosystems (freshwater river basins, estuaries, and sea) are intrinsically connected hydrologically and biologically. For instance, fish communities in an estuary typically share species with its adjacent freshwater ecosystem, and with its adjacent marine ecosystem, with diadromous species migrating across the three types of ecosystems. In addition, adjacent aquatic ecosystems are faced with some degree of similarity in environmental variables and pressures from human activities. However, different types of aquatic ecosystems are usually studied separately resulting in mismatching datasets and analysis of patterns and drivers. As a result, contemporary time series of biodiversity of fish communities in immediately adjacent marine and estuarine ecosystems are scarce, and linked analysis of such data sets are even scarcer. One example of a contemporary and adjacent time series is that of the Mondego estuary (Portugal, studied yearly since 2003) and of the continental shelf and slope (studied yearly since 1990, and with the current design since 2005). We analyse temporal changes in taxonomic, functional, and phylogenetic biodiversity of fish communities of the Mondego estuary-marine ecosystem, including different biodiversity indices, and model the relationship of these changes with environmental drivers (e.g. linked with climate change). The case study is proposed as a possible example for the same approach to be implemented in other areas.

S1O4 Fishing impact on the seascape connectivity influence on benthic species distributions

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Abstract

Composition of substrate is a primary structural driver shaping benthic species distributions in marine ecosystems. However, neighbouring context such as the heterogeneity and connectivity of the seascape can also determine the density and the probability of occurrence of species with close connections to the bottom. In this sense, bottom fishing trawlers is a long-lasting pervasive human impact on benthic ecosystems that does not only affect directly the species but also the ecological functions that the seascape connectivity has on the species distributions. Here, we apply network tools to calculate different substrate connectivity metrics (e.g. degree, closeness and betweenness centrality) and assess how fishing fingerprint alters their influence on the spatial distribution of several benthic species. To do, we perform a comparative exercise with information of contrasting regions off the Iberian Peninsula and across benthic species with different life history traits. We show that seascape connectivity can heterogeneously influence the distribution of species with positive and negative effects of connectivity metrics attending to their different spatial ecology. The study also supports our expectations that, under certain circumstances, fishing can buffer the influence of seascape connectivity on the spatial distribution. Our results can provide further mechanistic information to the field of spatial distribution modeling as well as strengthening the scientific basis that supports the spatial management of commercial fisheries.

S1O5 Using multidisciplinary tools to investigate global drivers of distribution and connectivity of rock lobsters

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Abstract

Human activities are affecting the processes that connect populations in marine ecosystems. Anthropogenic climate change is driving the redistribution of organisms and several marine species are shifting their ranges to maintain favourable environmental conditions. These changes are expected to restructure ecosystems and modify their functionality. Here, recent research using genomics, hydrodynamic modelling and species distribution modelling will be presented to illustrate the power of multidisciplinary tools to understand changes in distribution and connectivity patterns through space and time. Rock lobsters (*Jasus* spp.) are useful model organisms to study the role of historical climatic variations on connectivity. The six extant *Jasus* lobster species (*J. caveorum, J. edwardsii, J. frontalis, J. lalandii, J. paulensis and J. tristani*) have a long pelagic larval duration (up to two years for *J. edwardsii*) and the potential for extensive dispersal. However, all species have a narrow latitudinal distribution (~25° to 47°) in the Southern Hemisphere. Our studies reveal important effects of habitat and demographic processes on the recent divergence of *Jasus* spp lobsters. In addition, as water temperatures increase in accordance with anthropogenic climate change, we predict a southern shift in the distribution range of rock lobsters which could further reduce larval transport between populations and add complexity to fisheries management.

S1O6 Live trade and hatchery stocking induce inter-oceanic introgression in clawed lobsters

Authors: Charlie D. Ellis, Tom L. Jenkins, Kirsty L. MacLeod, Jamie R. Stevens

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Abstract

The European lobster (*Homarus gammarus*) is a large decapod crustacean endemic to the Northeast Atlantic and Mediterranean Sea that is a keystone species in biodiverse ecosystems, but overexploitation of their valuable inshore fisheries have led to extensive collapses of some regional stocks. Despite significant dispersal potential, primarily during their pelagic larval phases, lobsters exhibit a variety of forms of genetic structuring, from a phylogeographic break and sub-populations isolated by hydrographic and topographic barriers, to more subtle clinal variation along more open continental coasts. However, studies utilising highly-differentiated genome-wide molecular markers also demonstrate the impacts of twin anthropogenic activities to disrupt patterns of natural gene flow. Firstly, we evidence intraspecific relocations via historic trade and, more recently, restocking with hatchery-reared post-larvae, which have translocated lobsters beyond the extent of natural connectivity. Secondly, we evidence how the live import of the congener American lobster (*H. americanus*) for seafood marketing has led to hybridisation with the native European species and possible signs of establishment following its introduction to the wild across multiple regions. We discuss how this artificially-induced introgression threatens the conservation of vulnerable European lobster stocks, the livelihoods their fisheries support, and the wider biodiversity of inshore benthic assemblages.

S1O7 Evidencing Europe’s lost native oyster (*Ostrea edulis*) habitats

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Abstract

Aggregations of European flat oyster (*Ostrea edulis*) can form highly diverse biogenic habitat, but centuries of fishing pressure combined with disease and other problems led to this habitat becoming heavily depleted throughout its range and largely functionally extinct. The early loss of many wild oyster habitats has led to a major gap in our understanding of these habitats: what they looked like, where they used to occur, their extent, and which species were associated with them. This presentation describes efforts to identify relevant historical documentary sources from across Europe and extract information from these sources to uncover the past distribution, abundance, and characteristics of European flat oyster habitats prior to their decimation. Records spanning hundreds of years enabled us to map the distribution and extent of historical oyster habitats with varying degrees of confidence along the coastal margins of Europe. Our findings demonstrate that native oyster habitats were once highly abundant and were likely a dominant habitat in particular inshore and offshore locations. This talk will demonstrate the utility of the historical record and longer-term perspectives for guiding restoration ambitions as well as helping to pinpoint areas where past oyster habitat thrived.

S1O8 The effect of outfalls, sea level rise and reduction of river flow over chlorophyll-a and nutrient water quality indicators in the Tagus Estuary (Portugal)

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Abstract

Estuaries act as nursery for several species, including commercial species. However, these systems are also deeply affected by anthropogenic activities (both directly and by climate change). Phytoplankton is one of the main estuarine primary producers and responds to several environmental factors including nutrient concentration. It is affected by anthropogenic activities; thus, it is considered a good water quality indicator. In this work we assess how the phytoplankton and nutrient indicators vary in response to outfalls in the present days and simulate future responses of the estuarine environment to increase in outfall discharges (10% as it is expected for maximum population growth), sea level rise (0.5 m and 1 m) and reduction of river discharges (of 25% and 50%, simulating the increase in intensity of droughts). Our results show that outfalls deeply affect the Tagus Estuary nutrient concentrations, mainly during the low neap tides. However, no significant variation in the chlorophyll-a concentrations and phytoplankton composition were detected in response to such variation in the nutrient concentration, meaning the tested outfalls probably had little effect on the phytoplankton community. In relation to the simulations of future scenarios, no significant influence was verified with a 10 % increase in outfall discharge, besides a small increase in ammonium in the vicinity of the outfall. Sea level rise and reduction of river discharges lead to similar effects which mainly resulted from lower freshwater contribution to the estuarine water. Such effects included the reduction of nutrients and chlorophyll-a concentrations in the medium and upper estuary. As these modifications lead to changes in the phytoplankton community (probably both biomass and composition) a careful analysis of the effect over the estuarine environment must be performed.

S1O9 Migration dynamics and genetic divergence of co-occurring vent and seep macrofauna shed light on the conservation of deep-sea biodiversity

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Abstract

Deep-sea hydrothermal vents and hydrocarbon seeps are two spectacular biodiversity hotspots in the deep ocean, with one mainly located in tectonically active regions and the other along continental margins. With over ninety hydrothermal vents and seventy hydrocarbon seeps discovered, the Northwest Pacific has not only been recognized as an evolutionary hotspot for vent- and seep-endemic macrofauna, but also as a prospective target for deep-sea resource explorations, including mining of polymetallic sulfide from hydrothermal vents and extraction of gas hydrate from hydrocarbon seeps. These human activities can have huge impacts on these distinct habitats on our planet. Nevertheless, due to limited information on the life-trait history, population connectivity, and resilience potential of representative deep-sea organisms, it remains challenging to establish informed guidelines for the conservation planning of vent and seep ecosystems in the deep ocean. To fill such knowledge gaps, we have conducted large- scale population connectivity studies of two iconic deep-sea macrofaunal species, including the patellogastropod limpet *Bathyacmaea nipponica* and the munidopsid squat lobster *Shinkaia crosnieri*, which widely co-occur in both vent fields and seep areas in the Northwest Pacific. Combining population genomic tools with hydrodynamic modeling approaches, we unveiled their migration dynamics, genetic divergence, along with potential sources and sinks of gene flows. Our findings provided solid scientific evidence for the biogeographic units of these two deep-sea species in the Northwest Pacific, which will contribute to the conservation of deep-sea biodiversity and the development of management plans for vent and seep ecosystems in this region.

S1O10 Trends in Atlantic bluefin tuna (*Thunnus thynnus*) mixing proportions inferred from combined otolith chemistry and genetic data

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Abstract

The Atlantic bluefin tuna (ABT, *Thunnus thynnus*) is a large pelagic migratory species that lives mainly in the temperate ecosystem of the North Atlantic Ocean and adjacent seas. The management plan for ABT considers two management units (stocks) separated by the 45°W meridian, assuming that the western stock spawns in or near the Gulf of Mexico and the eastern stock in or near the Mediterranean Sea. Challenging this assumption, several studies have shown that mixing occurs between the two management areas, which results in uncertainties about the degree of connectivity between the two stocks with implications for stock assessment and management advice. Here, we have revised otolith stable isotope ($\delta^{13}C$ and $\delta^{18}O$) and genome- wide Single Nucleotide Polymorphisms (SNPs) genotype data from more than 1000 ABT individuals captured throughout the Atlantic Ocean (on both sides of the 45°W meridian) over the last 11 years. Results from both methods were integrated with a random forest approach and individual fish were assigned to their most likely population of origin (i.e., west or east). The contributions of the eastern and western populations to four different mixing areas in the Atlantic Ocean were estimated, and trends in connectivity patterns were assessed (e.g., catch-year, birth-year, area, age-class, sex). Preliminary results indicate year to year variation in the movement and exchange of ABT in mixing zones. The improved knowledge of the spatial dynamics of the species, will provide insights into the complexity and drivers of ABT stock mixing during the last decade, paving the way for informed management that ensures a sustainable exploitation of the species.

S1O11 How mechanistic food web modelling can inform marine functional connectivity in the context of climate change – a case study of the Portuguese continental shelf ecosystem.

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Abstract

Marine ecosystems worldwide, the functions and services they provide are affected by climate change. Increase in temperature, changing patterns in ocean currents, and productivity, are affecting the distributions of marine species globally. Due to increasing temperature northward expansion of marine species has been documented and an increasing number of studies confirmed an intensification of this trend in the next decades. In this study, we used the ecosystem food web model, Ecopath with Ecosim, to demonstrate how the Portuguese continental shelf ecosystem has changed over the last three decades, and how this ecosystem is expected to change under future climate predictions. The ecosystem indicators, that describe the ecosystem state, indicate that over the last three decades, the stability, resilience and biodiversity of this ecosystem have decreased, and future predictions show a continuation of this tendency. The main changes observed in this ecosystem were related to changes in the pelagic community that shifted from sardine, the main fishing resource, to other less valuable pelagic fishes such as chub mackerel. In this study, we also explore if, and to what extent, management strategies such as marine protected areas, essential habitat restoration and sustainable fisheries practices, can diminish or counteract expected changes. Ecosystem food web models such as Ecopath with Ecosim describe trophic flows between organisms within an ecosystem, therefore they can be useful to inform about marine functional connectivity, ecosystem functions and their services. As demonstrated in this study, these types of models can provide information about the future fate of ecosystems and marine species under future climate scenarios. Moreover, this information can support the strategic management of marine resources and marine ecosystems.

S1O12 Effects of bottom trawling on benthic-pelagic coupling by demersal predators

Authors: Rabanal I.[1], López-López L.[1], Ortiz J.J.[1], Rodríguez-Gutiérrez J.[1], Muñoz I.[2], Iglesias D.[1], Preciado I.[1]

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Abstract

Feeding movements are essential contributors to marine functional connectivity, as animals can move counter-gradient to feed redistributing biomass and nutrients. Among marine organisms, one of the functional groups having a well-known role in connectivity are demersal predators, which couple pelagic and benthic system integrating benthic and pelagic energy pathways across time. However, little is known on the effect of fishing, and particularly bottom trawling, on the benthic-pelagic coupling these animals perform. Trawling decreases benthic habitat diversity and complexity and as such, could potentially change demersal predators feeding toward non-benthic compartments. We test this hypothesis investigating the response of two species of megrim (*Lepidorhombus whiffiagonis* and *Lepidorhombus boscii*) feeding ecology to bottom trawling in the Southern Bay of Biscay (Northeast Atlantic), based on functional traits of the prey such as habitat and mobility. *L. whiffiagonis* and *L. boscii* are commercial species targeted by trawl fisheries with a mixed diet that includes both benthic and pelagic prey which makes it a good example to demonstrate the effect of fishing on benthic-pelagic coupling. Using 14 years of spatially resolved diet information, based on annual monitoring of megrim diets during the international bottom trawl surveys in the North Atlantic and Cantabrian Sea, we estimated the contribution of prey to megrims diet along its ontogeny in different habitat and mobility categories. Subsequently, we assessed space-time patterns in these prey categories under a wide range of fishing intensities using generalised additive models. Fishing effort was estimated through vessel monitoring system data, and aggregated to annual trawling intensity to match the resolution of our diet monitoring. Our results suggest an effect of fishing on benthic-pelagic coupling, particularly among the largest size classes of one of the species of megrim (*Lepidorhombus whiffiagonis*). However, these results might be species specific, with other demersal predators, particularly those with opportunistic or scavenging feeding behaviours, showing a different response to benthic trawling. These results will shed light on how the functional connectivity of a key bentho-demersal species can aid stock assessment and future management strategies.

S1O13 Monitoring introgressed alien genes left by human-mediated gene flow in sea squirts

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Abstract

Human-mediated translocations of species across oceans disrupt natural connectivity and create opportunities for hybridization between previously allopatric species. This is a major, although still understudied, outcome of marine biological introductions, which is well-exemplified by the recent introduction of the sea squirt *Ciona robusta* (native to the North Pacific) in the native European range of *C. intestinalis* (native to the North Atlantic). A recent population genomics study revealed an introgression event (i.e., gene flow) from the introduced to the native species. Further genomic work showed that the introgression is likely adaptive. It is thus required to survey the fate (i.e., increased abundance, spread) of the non-indigenous species, but also of introgressed alien genes in native populations. In this context, we developed an innovative cost-effective KASP multiplex genotyping approach to identify native, non-native and hybrid individuals as well as introgressed alleles. We aimed at determining if the introgression has increased in frequency and spread along the European Atlantic coasts as compared to observations made 10 years ago (i.e., 20 generations). For this, about 800 individuals of the two species were collected in 21 ports in France and the UK. The KASP method proved to be an effective approach to survey the impact of the introduction of an invasive species, here with the introgression of a native species. Introgressed alleles were indeed easily detected in ports where the introgression was previously found, showing its stability, as well as in new ports, suggesting it is spreading to other locations. Interestingly, field and eDNA surveys in the same locations suggested a decline of the non-native species. The introgressed invasive alleles might thus be a legacy of a disappearing invasive species.

S1P1 The Role of Human Impact in Updating The Marine Connectivity Model in The Bulgarian Black Sea Coast

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Balkan and Black Sea Business Institute - Regional Cluster "North-East"

Abstract

Since ancient times people's lives has always been associated with water ponds. The first civilizations have developed in coastal areas taking advantage of natural resources. Over the years, people have begun to have an adverse impact on the environment they inhabit, forming the second group of factors - those that are the result of human activity. Using the historical approach in their research the authors offer utilization coefficient of natural resources in the coastal area of Bulgaria. This ratio is in direct subordination to the duration of use of a given region and also duration and intensity of the impact of human factor and could help to create a map of areas with more or less exhausted natural resources along the Bulgarian Black Sea coast. This coefficient will contribute to a better understanding of the integrated management of coastal zones in Mediterranean and Black Sea countries. The report briefly discusses in chronological order the civilization periods in the history of the Bulgarian Black Sea coast. A review of climate changes affected the living conditions in the coastal marine area was made. A rating of anthropogenic effects lead to changes in natural resources in different historical periods was made as well. The attention of authors is focused on the development of civilization processes driven by natural resources of the area. In conclusion the authors try to summarize the sensitivity of human development from nature factors and integrated coastal zone management indicators and the important role of Blue Economy for sustainable development. It is recommended to use interdisciplinary and complex approach to understand better the past and to create a successful scenario for the future development of the coastal zones and human society.

S1P2 Thermal structure of Jurassic marine benthic assemblages determines ecological response to warming pulses

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Abstract

Marine assemblages are expected to undergo substantial reorganization under anthropogenic climate change but predictability and links to global extinction risk is unclear, especially with multiple stressors. Assemblage vulnerability to reorganization can be indicated by the thermal niches of its component species. To include empirical extinctions, we infer the thermal niches of Jurassic invertebrate species, based on observed distributions of fossils on paleoclimate maps, and assess species and assemblage responses over the Late Pliensbachian to early Toarcian transition. This was an interval of multiple warming pulses including an ocean anoxic event, the TOAE. We show that emigrants from a fossil assemblage after warming, including those species that went extinct, were most likely from the pool of species that were already close to their upper thermal limits before warming. Conversely, assemblage immigrants had warmer thermal niches than the assemblage pre-warming average. Evidence was weaker from regions strongly impacted by the spread of anoxic bottom waters, suggesting that additional stressors reduce the predictability of species' persistence or arrival based on their relative thermal preferences.

S1P3 Can the invasive seaweed *Asparagopsis armata* outcompete the resident *Ulva lactuca*?

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Abstract

Invasive species are known opportunists that take advantage of transient environments, often under abiotic stress. The red seaweed *Asparagopsis armata*, has been spreading worldwide due a high biomass buildup alongside a very toxic exudate. But what happens when this species encounters the opportunistic native green seaweed *Ulva lactuca*? To answer this, healthy thallus of *U. lactuca* were exposed to 3 concentrations (1, 2 and 3%) of *A. armata* exudate under laboratory conditions. Effects were assessed with an integrative approach through the evaluation of disturbances in primary productivity using Pulse Amplitude Modulated Fluorometry (PAM) together with oxidative stress and energetic metabolism related biomarkers. Specifically, DNA damage, lipid peroxidation (LPO), Electron Transport System Activity (ETS), carbohydrate, lipid and protein contents were quantified, and the Cellular Energy Allocation estimated. Significant differences could be detected in response to the growing exudate concentrations. *Asparagopsis armata* exudate induced significant stress to *U. lactuca*, indicating that it may not be able to prevent the spread of the invasive seaweed.

S1P4 Modelling the Future Changes in the Fish Stocks of the Black Sea under Climate Change and Fisheries Exploitation

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Abstract

Various ecosystem models have been developed to investigate the dynamics of marine fish communities affected by natural and anthropogenic pressures. They have provided a better understanding of the food web dynamics. The aim of this study was to investigate the possible future changes in the Black Sea fish stocks under climate change and fisheries exploitation until the end of the 21st century. To this end, we used the individual-based model OSMOSE (Object-oriented Simulator of Marine Ecosystems Exploitation), which provides opportunistic predation based on size and spatial co-occurrence between predator and prey. The dynamics of eight commercially important fish species, anchovy, sprat, horse mackerel, whiting, red mullet, turbot, bluefish, and bonito, were examined under two scenarios, a hindcast scenario for the years 2000-2019 and a future scenario for the years 2080-2099 representing the IPCC RCP 6.0 climate scenario. Results showed that there will be a significant decrease in the populations of all fish species except anchovy, and the mean sizes of all fish species except anchovy, horse mackerel, sprat and red mullet will decrease by 2100. Our study contributed to a better understanding of future changes in the Black Sea fish stocks under climate change and fisheries exploitation; hence, it can help to develop mitigation plans against the negative ecological and economic impacts of the predicted changes.

S1P5 Coral community connectivity in the South China Sea along the coast

Authors: Haoya Tong, Meixia Zhao, Ting Xu, Guowei Zhou, Pei-Yuan Qian

The Hong Kong University of Science and Technology

Abstract

The South China Sea, which is part of the Coral Triangle, is abundant in various coral species and fishery resources. However, the coral communities in the region have been declining rapidly in recent years due to rising anthropogenic activities and tourism along the coast. Additionally, little is known about the connectivity of the coral populations in the area and how human activities might impact them. In the present study, we examined six iconic coral species from the area, including different growth forms and levels of stress tolerance: *Acropora digitifera* (branching, sensitive), *Galaxea fascicularis* (massive, tolerant), *Platygyra carnosus* (massive, sensitive), *Porites lutea* (massive, tolerant), *Montipora peltiformis* (leaf, sensitive) and *Pavona decussata* (leaf, tolerant). By looking at the genetic population structure and gene flow level of these corals in the area, we discovered varied population characteristics of different coral species, and which coral populations may be more affected under human impacts. The majority of studied coral species in the South China Sea are self-sufficient, although protection measures are still necessary for the source coral populations there. This study provides theoretical framework for regional marine conservation and is important for conducting future development strategy.

S1P6 Sharks in the Anthropocene: a systematic map of global research efforts

Authors: Catarina Pereira Santos [1, 2], Maria Rita Pegado [2], Catarina Frazão Santos [3 2, 1], Rui Rosa [3, 2]

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Abstract

Over the past centuries, humans have been transforming the biogeophysical landscape that carried species evolution over the geological past. Sharks and their relatives represent one of the lineages struggling to keep pace with this new set of challenges, with over a third of their species under risk of extinction. Increasingly aware of the ecological and socioeconomic value of this group, researchers have been striving to evaluate the scale of anthropogenic threats and how to mitigate its impact. Here, recognizing the challenges implicit to such endeavour, we implement a hierarchical systematic mapping approach to methodically scout and quantitatively describe the scientific landscape aiming to assess the effects of anthropogenic pressures over sharks, evaluating how these trends have evolved over time and are distributed across both spatial and biological scales. A clear shift in the scientific discourse from “sharks as a threat” to “sharks under threat” can be observed. Further, although fisheries and habitat degradation have long been recognized as the most pressing threats to this group, a recent relative increase in the assessment of typically sub-lethal threats, namely pollution and climate change, can also be observed, with distinct methodological profiles across threat categories. Moreover, a strong geographic bias in threat assessment efforts is evident and, remarkably, misaligned with diversity hotspots and conservation targets. Through this approach we hope to set the stage for the integration of different avenues of research which, applying distinct approaches and methodologies, ultimately aim towards a similar goal - to understand how sharks may fare in the oceans of tomorrow.

S1P7 The role of physical and human activity derived connectivity in the spread of *Rugulopteryx okamurae* in the Mediterranean basin: potential application for risk assessment.

Authors: Muñoz, M.[1], Hidalgo, M. [2], Reul, A.[1]

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Abstract

The invasive brown alga, *Rugulopteryx okamurae*, was cited first in 2002 in the Mediterranean Sea in the Thau coastal lagoon (Occitania, France) and then again in 2015 in the Strait of Gibraltar, with never seen growth rates and up to 80% of coverage on hard rock substrate (García-Gómez. et al., 2020). Affecting coastal ecosystems and socioeconomic fields such as extractive fishery and tourism, causing costs of 1.2 million € in nine months (ECRO, 2022) among removing landed biomass on the beach and loss in the extractive fishery sector. After its first description in the strait of Gibraltar, *R. okamurae* spread eastward along the Mediterranean coast, and have reached already Calanque National Parc (Marseille France) (Ruitton *et al.,* 2021) Apart of the ecologic damage, due to the elevate socio-economic losses special interest is paid to the expansion of *R. okamurae* and possible measures to mitigate their impact. One of them is to prevent arrival and local spread of *R. okamurae*. Spread of *R. okamurae* is naturally driven by sea currents and difficult to avoid. However, as invasive species with very high biomass it also obstructs fisher net, and fishing activity transport *R. okamurae* facilitating outspread. Here we show a first estimation of physical connectivity and fishery derived connectivity trough bottom trawling among suitable habitat of *R. okamurae* identifying the area at highest risk for invasion in the future and possible measure to limit fishery derived connectivity in order to avoid or reduce negative socio-economic impacts in areas still free of this invasive species.

García-Gómez, J.C. *et al.*, 2020. From exotic to invasive in record time: The extreme impact of Rugulopteryx okamurae (Dictyotales, Ochrophyta) in the strait of Gibraltar, Science of The Total Environment, Volume 704. https://doi.org/10.1016/j.scitotenv.2019.135408.

ECRO, 2022. Estrategia de control del alga Rugulopteryx Okamurae en España. 2022. https://www.miteco.gob.es/es/biodiversidad/publicaciones/estrategia_rokamurae_cs_28072022_tcm30-543560.pdf

Ruitton, S. *et al.*, 2021. Rapid Spread of the Invasive Brown Alga Rugulopteryx okamurae in a National Park in Provence (France, Mediterranean Sea). Water 2021, 13, 2306. https://doi.org/10.3390/

Theme session 2 – Responses of marine connectivity to environmental extremes and incidental human impacts

22 May 2023 – 23 May 2023

Conveners:
Lucía López López, IEO-CSIC, Spain
Susanne Tanner, MARE/University of Lisbon, Portugal
Filip Volckaert, KU Leuven, Belgium

Incidental human impacts (e.g. oil spills, marine infrastructures) or increasingly frequent extreme events resulting from climate change (e.g. increasing frequency and severity of storms, marine heatwaves) are known to have profound and long-lasting impacts on the structure and functioning of marine ecosystems. Such impacts can also alter recurrent connectivity pathways of marine organisms and/or alter the functional implications of connectivity.

This session calls for studies assessing the implications of incidental impacts and extreme events on connectivity processes. These may include studies that are field-, laboratory-, or model-based, or any combination of these. Research topics include, but are not limited to, movement ecology, behavioral ecology, biogeochemical cycles, food web studies, and the development of analytical methods and tools to investigate these processes.

S2 Keynote: Climate change, hurricanes and marine connectivity

Keynote: Emmanuel Hanert
UCLouvain, Earth and Life Institute, Belgium

Abstract

Climate change poses an existential threat to marine ecosystems. A warmer and more acidic ocean increases larval mortality, alters the competence acquisition dynamics, changes larval vertical swimming behavior and increases the intensity of hurricanes. All these processes influence marine populations connectivity, a process fundamental to their recovery following disturbances. Here we quantify the impact of these different processes on coral and crab larvae connectivity by using a high-resolution ocean circulation model coupled with a wave model to simulate the effect of major hurricanes, such as Irma that struck Florida coral reefs in Sept. 2017. We show that the increased larval mortality and reduced competency duration due to ocean warming reduce habitat connectivity, hampering recovery after disturbances and reducing the spread of warm-adapted genes. Similarly reduced seawater pH leads to a deeper distribution of crab larvae, hence reducing the distance they can travel, increasing self-recruitment and leading to a more fragmented community structure. While being a brief event, the passage of a hurricane however significantly increases the probability of long-distance exchanges, creates new connections, and reshuffles the usual community structure. Hurricanes can therefore both promote coral resilience by diversifying larval exchanges but also speed-up the propagation of coral diseases. Our results suggest that protection measures will be more effective locally, and may require reducing spacing between protected areas. As hurricanes become more intense and probably also more frequent, they will increase variability within marine ecosystems and hence make their management less predictable.

S2O1 Quantifying population connectivity during a climate-driven northern range expansion

Authors: Cataixa López[1], Benjamin Daniels, Andy Lee, Crow White, Mark R. Christie, Jean M. Davidson, Paul Anderson, Rob J. Toonen

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Abstract

Rising ocean temperatures, combined with alterations in ocean currents, are enabling marine species to expand poleward and establish populations beyond their historical distribution limit. In this context, the importance of understanding population connectivity for effective management is obvious. However, despite decades of research, our understanding of how marine populations are connected through space and time remains unclear for most species. Our project seeks to develop a novel approach to empirically quantify functional connectivity using the kelp forest gastropod (*Kelletia kelletii*), that expanded its range northward during a major El Niño event and has established a population outside its historical range as a result. We first performed simulations to determine the types and number of loci that provide the greatest power to resolve connectivity in population genetic and assignment testing approaches. We then identified differentially expressed genes using transcriptomic comparisons from common-garden laboratory crosses between historical and range-expanded populations. We are now working to combine analyses of putatively neutral and differentially expressed SNP loci between the historical and expanded range. Leveraging the resolution of this genomic data, we will assign annual recruits back to their source populations with the hope of fully resolving population connectivity across the entire species' range (~1600km). With climate change causing increasingly common and dramatic shifts in marine species distributions, understanding connectivity is essential to manage and conserve the health of marine ecosystems and the services they provide to human populations. This study will provide a novel framework for identifying the most informative genetic markers and empirically quantifying population connectivity in a broadcast spawning coastal marine species.

S2O2 Effects of biogeographic range shifts on mudflat ecological functioning in the subtropics: Projecting functional change

Authors: Bryony A. Caswell [1,2]*, Navodha G. Dissanayake[2], Christopher L. J. Frid[2]

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Abstract

A growing volume of evidence shows that the broad-scale biogeographic redistribution of species is occurring in response to increasing global temperatures. Changes in species biogeographic ranges raise questions surrounding the ecological response of communities with altered and, often novel new species combinations and their ecological functioning. The present study documents poleward movements of eight species of nominally ‘tropical’ macroinvertebrates (molluscs, polychaetes, crustaceans and foraminifera) from intertidal mudflats on the southeast coast of Australia dating from the 1960s. The worm and mollusc species moved at 70–300 km decade-1 faster than the Australian marine fauna more generally. We used biological traits analysis to investigate how the observed species range changes might have impacted mudflat ecosystem functioning, and to predict the possible impacts of further poleward movements of the tropical taxa. Our models suggest that the changes to date, and those likely to occur in the near future, are within the envelope whereby ecological functioning is maintained by functional compensation and redundancy within the assemblage. However, under the most extreme scenario the replacement of temperate by tropical taxa resulted in major changes in potential ecological functioning with impacts for nutrient cycling and c-cycling, undermining the potential of these mudflats to continue to deliver valuable ecosystem services. Exploration of the biological traits of the receiving communities and the shifting species can help us to project future scenarios, especially if supplemented by observational and experimental research on non-native invasive species ecology.

S2O3 Rare long dispersal events may facilitate current and future marine connectivity in a cold-water octocoral, pink sea fan (*Eunicella verrucosa*)

Authors: Kirsty Louise Macleod

University of Exeter, England, United Kingdom.

Abstract

This study combines genomic tools and oceanographic particle modelling to examine population connectivity in a temperate, soft coral – the pink sea fan, *Eunicella verrucosa.* Taking this further, this study is complemented by a future climate-scenario species distribution model (SDM) and an on-going thermal *ex situ* common-garden experiment to better understand, and predict, how pink sea fan marine connectivity may change in response to human-induced oceanic warming. Patterns of genetic connectivity show a clear geographic cline, partitioning into six genetic clusters: Ireland, Britain, France, Spain (Atlantic), Portugal and Spain (Mediterranean), characterised by a strong signal of isolation-by-distance (IBD) ($r^2 = 0.78$, $p<0.001$) which persisted across the Mediterranean Atlantic divide. Particle trajectory patterns show a high degree of inter-annual variation in particle displacement distance, suggesting that range-wide IBD could be facilitated by rare, longer dispersal events sufficient to maintain gene flow. In range-edge sites, longer trajectories show potential stepping-stone connectivity to more northerly regions where populations are currently not present. The genetic data complements findings from the SDM and indicates that projected climate changes will facilitate marine connectivity across the UK and northwest France, and support a northward range expansion, although this would be conditional on other factors, such as dispersal, availability of suitable substrate and interspecific competition. *E. verrucosa* acts as a key ecological substrate for many epifauna and contributes to the three-dimensional structural complexity of temperate benthic ecosystems, however, this also renders populations vulnerable to physical disturbance. As a result, this species is legally protected in the UK and a designation feature for Marine Protected Areas (MPAs); globally it is listed as 'vulnerable' on the IUCN Red List. Characterising patterns of connectivity will directly aid in advising both current and future conservation policies for this species, such as future MPAs, and better predict its response to climate-change.

S2O4 Evaluating resiliency and functional connectivity of early life stages of invertebrates within a southern African urban coastal system under an era of climate change

Authors: Kerry-Ann van der Walt[1], Paula Pattrick[2], Seshnee Reddy[1], Francesca Porri[1]

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Abstract

Estuaries and rocky shores are fundamental ecosystems for biodiversity, often acting as nurseries of larvae and juveniles of marine organisms and settlement areas for intertidal species. Anthropogenic-related activities and effects such as urbanisation, rising sea levels and increasing mean ocean temperatures, however, may be placing ecological and physiological pressure on the early life stages recruiting into coastal systems. Multifaceted coastal defences, specifically, may carry negative connotation as it often results in decreased and fragmented abundance of marine coastal biodiversity. The aim of this study was therefore to first quantify the ecophysiological challenges encountered by early life stages associated with urban infrastructures. To achieve this, zoeal and megalopal life stages of selected brachyuran larvae (*Pinnotheres* sp. and *Hymenosoma orbiculare*) were collected from two artificial microhabitats, jetties and seawalls, within an urban South African coastal system upon which oxygen consumption rates of individual larvae were then measured using an optical fluorescence-based oxygen meter in a 24-well glass microplate at five test temperatures which included 11, 15, 19, 22, and 25^{o}C. Preliminary results indicated that thermal performance at the zoeal life stage for both species may be more vulnerable to high temperatures increasing from 22^{o}C from both artificial habitats. This suggests that, physiologically, due to its stenothermic nature, the zoeal life stages may be more vulnerable than the megalopal life stages to increases in thermally variable events such as marine heatwaves which are expected to increase in frequency and intensity in this region. Furthermore, especially considering the urban context of these results, we may be facing potential bottlenecks/retention areas for the successful recruitment of these species at the megalopal stage.

S2O5 Onset of the Mediterranean West-to-East biodiversity gradient

Authors: Konstantina Agiadi[1]*, Niklas Hohmann[2], Elsa Gliozzi[3], Danae Thivaiou[4], Marco Taviani[5], Francesca Bosellini[6], Giovanni Bianucci[7], Alberto Collareta[7], Laurent Londeix[8], Costanza Faranda[3], Francesca Bulian[9], Efterpi Koskeridou[4], Francesca Lozar[10], Alan Maria Mancini[10], Stefano Dominici[11], Pierre Moissette[4, 12], Ildefonso Bajo Campos[13], Enrico Borghi[14], George Iliopoulos[15], Assimina Antonarakou[4], George Kontakiotis[4], Evangelia Besiou[4], Stergios D. Zarkogiannis[16], Mathias Harzhauser[17], Francisco Javier Sierro Sànchez[9], Marta Coll[18], Iuliana Vasiliev[19], Angelo Camerlenghi[20], Daniel García-Castellanos[21]

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Abstract

Physical connectivity between marine basins facilitates population exchange and hence controls biodiversity. The Mediterranean Sea is a semi-restricted basin with only a small two-way connection to the global ocean, and it is a region heavily impacted by climate change and biological invasions today. The massive migration of non-indigenous species into the basin through the Suez Canal, driven and enabled by climate warming, is drastically changing Mediterranean biodiversity. Understanding therefore the origin and cause(s) of pre-existing biodiversity patterns is crucial for predicting future impacts of climate change. Mediterranean biodiversity exhibits a west-to-east decreasing gradient in terms of species richness, but the processes that resulted in this gradient have only been hypothesized. By examining the fossil record, we provide evidence that this gradient developed 5.33 million years ago at the end of the Messinian Salinity Crisis, and it was therefore caused by the re-population of the basin by marine species with a dominating western source at the Mediterranean–Atlantic gateway.

S2O6 Ocean deoxygenation drives midwater fish decline in the ancient Eastern Mediterranean

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Abstract

Midwater fish are key players in ocean food webs and are of highest importance for carbon transport through performing diel vertical migration, therefore they play a crucial role for marine functional connectivity. Ocean deoxygenation caused by anthropogenic warming is hypothesized to pose severe threats to the mesopelagic fish community by enhancing physical stress and changing prey-predator relationships, thus having long-lasting impacts on the structure and functioning of marine ecosystems. Here we use Holocene sediment cores to show that there was a marked decline of midwater fish fauna during times of severe ocean deoxygenation, in agreement with modern observations and models of future climate change. Our Holocene fossil otolith time series from the Eastern Mediterranean Sea indicates extremely low overall abundances of mesopelagic fish during Sapropel deposition, a time when bottom to mid-waters were highly anoxic, and surface waters were remarkably productive. Fish species adapted to the epipelagic habitat like the European anchovy (*Engraulis encrasicolus*) and the Silvery lightfish (*Maurolicus muelleri*), dominate the otolith record. After reoxygenation, mesopelagic fish abundance increases, with lanternfish (myctophids) being the most dominant family from mid-Holocene to present times. Our results serve as a past analogue, demonstrating the negative response of midwater fish fauna to ongoing intensification and expansion of OMZs over coming centuries. A sharp decline of mesopelagic fish abundance would have major impacts on marine fisheries, marine conservation, ocean food web structure and carbon storage capacity, with adverse knock-on effects for global marine functional connectivity.

S2O7 Changes in complex rocky reef food-web due to the human threats: diversity-stability dynamics.

Authors: Sofia Henriques [1], Marisa Batista [1], Rita Vasconcelos [2], Susanne Tanner [1], Ferenc Jordan[3], Marta Coll[4], Hilmar Hinz [5], Manuel Hidalgo[6]

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Abstract

Rocky reef habitats support very complex food-webs given the high diversity of resources (e.g. shelter, food) provided for numerous species. Most human pressures induce simplification of complex habitats and communities, which in turn alters species' interactions (direction and strength) and therefore may change the structure and dynamics of the entire food-web. To investigate the diversity-stability dynamics of a highly complex food-web (i.e. high species diversity is expected to increase stability), we first develop a baseline ecological model with data from rocky reefs of a no-take zone in Arrábida Marine Protected Area in Portugal. We then define alternative scenarios based on documented changes in marine assemblages due to natural and anthropogenic pressures (i.e. fishing, nutrient enrichment, marine traffic and ballast water exchange, temperature increase, acidification). Ecological network analysis was used to quantify, for alternative scenarios and different levels of pressure, the topological and dynamic properties of the network (e.g. indicators such as pathway indices, production, consumption, dominance, keystoneness, redundancy) and use the differences to estimate the overall network resilience. Finally, based on these results we identify sensitive and accurate network indicators of human-induced changes (e.g. indicator species, sensitive functional groups) and respective tipping points (i.e. warning thresholds), contributing for improving the efficiency of monitoring of rocky reef habitats.

S2O8 Anchovy dispersion patterns under anomalous oceanic conditions in the northern Iberia

Authors: Ana Teles-Machado[1,2], Sandra Plecha[2,3], Álvaro Peliz[2,3], Susana Garrido [1,4]

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Abstract

Anchovy recruitment is thought to be largely controlled by environmental conditions experienced by the early life stages (eggs and larvae). The abundance of the European anchovy has increased sharply from 2015 and has shown an increasing trend since then. It is unclear if the increase of anchovy abundance off the west coast was a result of dispersal from close recruitment areas, higher survival of the early life stages due to favorable environmental conditions, or both. In this study, a set of different models are used to simulate the dispersion and survival of anchovy early life stages in the Iberian Current System. A high-resolution simulation (IBv2.0) with the hydrodynamic model ROMS provides the oceanographic fields that are used as background for the lagrangian simulations performed with the model Parcels coupled to an Individual Based Model (IBM) of anchovy eggs and larvae. The IBM is developed based on the relationship between vital rates and key oceanographic factors, available in the literature and obtained from laboratory-controlled experimentation, it simulates the different early life stages of anchovy considering the effects of temperature and food availability on growth, survival, and development throughout ontogeny. The lagrangian/IBM models are used to study the dispersal of anchovy eggs and larvae during the anchovy spawning season and known spawning grounds off Iberian waters. The dispersion patterns are obtained for the years that preceded the increase in the recruitment strength observed off western Iberian to evaluate a possible connectivity between Western Iberia populations with either the South Iberia (Gulf of Cadiz) or the Bay of Biscay populations, during the egg and larval stage. Results show that during 2014 and 2015, a large number of the eggs/larvae deployed in the Bay of Biscay area were transported eastward along the Northern Iberian margin due to an anomalous upper-ocean circulation pattern, with stronger and persistent eastward currents. Additional experiments deploying eggs in the Cantabrian sea show that a large part of them are transported to the west coast. This anomalous upper-ocean circulation pattern seems to have increased the advection of eggs/larvae along northern Iberia and are a possible explanation for the sudden increase in the anchovy abundance off western Iberia.

S2O9 Potential impact of marine heatwave on population structure of sardine in the western North Pacific and its marginal seas

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Abstract

Sardine in the western North Pacific and the Sea of Japan supports one of the largest sardine fisheries in the world. Although the sardine is assumed to consist of two self-sustaining subpopulations in the Pacific and the Sea of Japan, biological evidence for this structure is severely limited. In 2014 and 2019, sardine schools in the Sea of Japan, which come to coastal areas each spring to spawn, were barely observed, and fishery catches and abundances of eggs declined to about one-tenth of the previous year. In 2015 and 2020, however, schools of sardines appeared in spring, containing age-1 fish hatched the previous year as usual. These observations not only indicated significant shifts in sardine migration patterns in 2014 and 2019, but also called into question the origin of the recruits in the Sea of Japan. Here, based on biogeochemical approaches, we show that sardine in the Sea of Japan do not form a self-sustaining subpopulation and most adult fish there likely originate from the Pacific. Analyses of stable oxygen isotope ratios in otoliths from over 350 individuals and stable carbon and nitrogen isotope ratios in eye lens cores from over 1900 individuals showed that isotope values were remarkably different between juveniles and adults in the Sea of Japan and similar between juveniles in the Pacific and adults in the Sea of Japan. Sea surface temperature analysis also showed that the southern Sea of Japan had been hit by severe marine heatwaves in the summer of 2013 and 2018. Unusually high summer sardine catches were observed near the boundary between the Sea of Japan and the Pacific Ocean in the summers of 2013 and 2018, implying that the heatwave caused Pacific immigrants to return to the Pacific, and not enter Sea of Japan again in 2014 and 2019.

S2P1 Population dynamics changes of invasive round goby in the Baltic Sea coast of Latvia

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Abstract

For marine invasive species, the most important pathway of introduction is shipping, and round goby is not an exception either. Due to increased global trade ballast waters were the longest-distance vector for small-size round gobies and fertilized eggs from the Ponto-Caspian region to the Baltic Sea ports. Last 30 years the round goby has spread in all sub-basins of the Baltic Sea. Based on catches, round goby population density is high, becoming the dominant species in coastal fisheries in several countries. Despite the importance of this species abundance of round gobies is unclear. During the last 10 years, the commercial catch on the coast of Latvia has increased more than 300 times. To assess the impact of fishing on population dynamics from the Latvian coast since 2014 have collected biological samples from commercial and scientific catches. It was found that in the Gulf of Riga round gobies body size and average age parameters in catch are lower than on the Latvian coast. However, in recent years, these body size differences are decreasing, indicating the stabilization of the population in both regions. Based on biological information was made the first attempt to assess the round goby population on the Latvian coast. The obtained stock assessment is approximate because when assessing the dynamics of population parameters with different models, different trends and levels of change were found. From 2014 to 2020 fishing mortality increases more than ten times (from 0.02 to 1.22). As result growth dynamics of spawning stock biomass and recruitment decreased more than three times. The stock of round goby on the coast of Latvia is expected to decline in the coming years. This population dynamic changes indicate that commercial fishing effort is a general mechanism to provide stabilization of round gobies invasion in the Baltic Sea coast of Latvia.

S2P2 Simulating fisheries management strategies in the Moroccan Mediterranean Sea ecosystem using Ecopath model

Authors: Salma Aboussalam, Karima Khalil, Khalid Elkalay

Essaouira School of Technology, Cadi Ayyad University, Morocco.

Abstract

For a better description of the structure, functioning and state of the Moroccan Mediterranean Sea ecosystem, an Ecopath mass balance model has been applied. Based on 31 functional groups, the model contains 21 fish, 7 invertebrates, 2 primary producers and one detritus group to explore trophic interaction. The average trophic transfer efficiency for the whole system was 23%. Total primary production and total respiration were calculated to be >1, suggesting that more energy is produced than breathed in the system. The structure of our system is based on high respiration and consumption flows. Indicators of ecosystem stability and development showed low values of the Finn cycle index (13.97), system omnivory index (0.18), and average Finn path length (3.09), suggesting that our system is disturbed and its trophic structure is more linear than networked. The key index and mixed trophic impact analysis indicate that other demersal invertebrates, zooplankton, and cephalopods have a huge impact on the other groups and are recognized as keystone species.

S2P3 Exploring the potential for oyster aquaculture to remediate biodiversity loss in oyster reef habitats using non-destructive environmental DNA sampling

Authors: Laura A. Givens, Brian R. Silliman, Thomas F. Schultz

Duke University, Durham, North Carolina.

Abstract

Bivalve aquaculture has been increasingly implemented on the US East Coast as a fisheries supplement to dwindling and overfished natural oyster reefs. However, the installation of oyster farms also changes the structure of the habitat, introducing hard 3-D structure to soft sediment areas and leading to possible carryover effects on the marine community utilizing that space. Although the rapid increase in aquaculture production has been associated with negative environmental impacts, the potential positive impacts on community diversity are still unknown. In this study, we evaluate the capacity of small-scale oyster aquaculture to provide habitat quality and foraging potential for a diverse biological community. Here, we introduce a method to incorporate non-destructive broad-spectrum eDNA metabarcoding and rapid, low-cost third-generation Nanopore sequencing to record community composition using surface water samples collected biweekly from April – November 2021 at six sites in North Carolina. Community composition identified at small-scale aquaculture facilities indicate that these sites do play host to a spectrum of organisms, picking up presence of vertebrates, small invertebrates such as annelids and bryozoans, and mobile organisms such as crustaceans and gastropods. We found that third-generation sequencing was an effective method to identify biological composition of aquatic communities. Our findings show potential avenues to expand understanding of ecosystem service provisioning to non-traditional sources like aquaculture that could be taken into consideration when developing local restoration action plans. Furthermore, the ability to use Nanopore sequencing in combination with eDNA analysis can reduce the need for destructive biodiversity sampling and increases the toolkit available for conservation and restoration agencies to answer ecological questions.

S2P4 Human impacts towards coastal systems: pharmaceuticals flow in estuarine food webs

Authors: Irina A. Duarte[1], Jerker Fick[2], Henrique N. Cabral[3], Bernardo Duarte[1,4], Vanessa F. Fonseca[1,5]

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Abstract

Directly linked with human presence and activities, the continuous release of pharmaceuticals into the aquatic environment is a current topic of major concern. Pharmaceuticals are ubiquitous in the aquatic environment and its pseudo-persistency and potential deleterious effects lead to their classification as emerging contaminants. Pharmaceuticals may interfere with essential biological processes, such as behaviour, development or reproduction, potentially threatening species fitness and survival and ultimately affecting population dynamics and connectivity. Moreover, they bioaccumulate and can be transferred along trophic webs. Highly populated areas such as coastal systems are important recipients of wastewater discharges, the main source of pharmaceutical contamination. With increased access to pharmaceuticals and following population growth, particularly in coastal areas, it is therefore paramount to determine the potential impacts and associated risk of these emerging contaminants on coastal ecosystems. In this context, this study aimed to investigate the occurrence, bioaccumulation and biomagnification of multiple pharmaceutical residues along an estuarine trophic web, including producers, primary consumers and multiple fish species. Specifically, samples of surface water, sediments, suspended particulate matter, plankton, plants, various invertebrates, as well as multiple tissues from different fish species (e.g. brain, muscle, liver), were collected from highly urbanized Tejo estuary, in Portugal. Stable isotope analysis was performed in the different estuarine compartments to determine trophic web structure and pharmaceuticals quantified via liquid chromatography tandem mass spectrometry (LC-MS/MS) in all trophic levels. The results provided new insights on pharmaceuticals occurrence, bioaccumulation and biomagnification patterns, and are discussed in the context of environmental risk focusing on the implications to estuarine and marine populations.

S2P5 Food web connectivity and contamination flow in a tropical urbanized estuary in West Africa

Authors: Celso Paulo[1], Renato Mamede[1], João Carreiras[1], Carmen Santos[2,3], Bernardo Duarte[1,4] & Vanessa F. Fonseca[1,5]

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Abstract

Diogo Cão bay is a large transitional system, located in the Zaire province, northwest of Angola (West Africa). The Congo River, the second largest river in the world, followed only by the Amazon, discharges into the bay. Due to its hydrodynamic protection towards ocean wave energy, the estuarine system becomes a suitable location for urban and industrial development. Main anthropogenic activities in the bay include oil and gas exploration, dredging, harbor, wastewater discharge, and fishing. Nevertheless, environmental features make this estuary a suitable area to harbor a large tropical ecosystem bordered by mangrove forests and inhabited by several species of fish and invertebrates. This study aimed to establish a connectivity network between biotic compartments along the trophic web, whilst describing the contaminant flow within this ecosystem, considering biotic and abiotic compartments. Biotic and abiotic compartments were surveyed along the whole estuarine system aiming to provide a complete picture of the trophic connectivity between compartments. Due to the marked biseasonal climatic features of this area, samples were collected during dry and rainy periods (sediment, water, mangrove leaves, invertebrate and various fish species). Trophic web structure was determined via stable isotope analyses, and legacy contaminants were determined by means of untargeted Total X-ray Reflectance Fluorescence spectroscopy (TXRF). Results are discussed in terms of connectivity between biotic and abiotic compartments, their trophic flow and also compared with contamination indexes attained for similar tropical systems.

S2P6 Response of the Mediterranean Sea billfish fauna (Teleostei, Istiophoridae) to the Messinian marine disruption

Authors: Carlos De Gracia[1,2,3]; Dayenari Caballero-Rodríguez[3], Eduardo Villalobos-Segura[1]; Faviel LópezRomero[1]; Gustavo Ballen[4] & Jürgen Kriwet[1]

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[4]School of Biological Behavioural Sciences, Queen Mary University of London, United Kingdom.

Abstract

Landscape connectivity determines the degree to which landscapes promote or impede movements of individuals, which consequently results from the interaction between the landscape structure itself and the vagility of species. In the open ocean, billfishes are among the largest megafaunal predators and are one of the most functionally unique species in pelagic ecosystems. Billfishes play a critical role regulating oceanic ecosystem structures, functions, and stabilities. Due to their highly migratory nature, billfishes require large areas to perform corresponding life histories. In the Mediterranean Sea, the fossil record of billfishes shows that it was a diversity hot spot. Today, however, only the swordfish and the small Mediterranean spearfish are the only permanent residents. Istiophorid billfishes were present during the late Miocene, but gradual shallowing and narrowing of the Gibraltar strait caused by the mantle-resisted slab dragging changed the environment from an oceanic corridor to a landlocked basin causing the extirpation of larger species (>300 cm) from ~8.2 to 5.33 million year (Ma). Smaller istiophorids seem to be more resilient but during the Messinian Salinity Crisis, between ~5.97– 5.33 Ma, all billfishes species, with no exceptions, vanished. The Mediterranean basin was refilled by the Zanclean Megaflood and the oceanic corridor was restored as also shown by fossil billfishes found in the western Mediterranean basin. The hypersaline conditions remained longer in the eastern basin and the equalization of the salt concentrations between the eastern and western basins increased the overall salinity to ~38o/oo in the entire Mediterranean. This incompatible tolerance regimen for most istiophorids caused the final extirpation of the larger species from the entire basin. Here, we evaluate the landscape connectivity of billfishes in the Mediterranean – Atlantic gateway during the Mio-Pliocene and show how the mantle-resisted slab dragging drove an environmental change that resulted in a regional extinction of large-sized billfish species.

Theme session 3 - Human impacts on species phenology and seasonality in marine connectivity

23 May 2023

Conveners:

Manuel Hidalgo, IEO-CSIC, Spain
Antonina do Santos, IPMA, Portugal
Filipe Martinho, CFE-University of Coimbra, Portugal

Marine ecosystems are characterized by strong seasonal variability in productivity and critical ecological processes across multiple trophic levels, shaping population and ecosystem dynamics. Climate change is known to substantially shift the timing of key seasonal processes, while supplementary human pressures can also impact functional connectivity.

This session calls for studies assessing impacts on connectivity processes through direct or indirect human-induced alteration of the timing of environmental and/or ecological seasonal events.

S3 Keynote: Northeast Arctic cod offspring survival resulting from spatial-temporal variation in spawning

Keynote: Clarissa Akemi Kajiya Endo

Authors: Clarissa Akemi Kajiya Endo[1,2], Morten D. Skogen [2], Leif Christian Stige [4, 5], Solfrid Sætre Hjøllo [2] and Frode B. Vikebø [2]

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[3] Institute of Marine Research, Norway (IMR)
[4] University of Oslo
[5] Norwegian Veterinary Institute

Abstract

The Northeast Arctic cod (*Gadus morhua*) inhabits the Barents Sea and perform extensive migrations to spawn at banks along the Norwegian coast. Climate change and harvesting pressure result in temporal and spatial variability in spawning and thus in offspring ambient drift conditions, resulting in variable survival of offspring and thereby in recruitment. In this study, coupled biophysical model simulations were used to analyse different scenarios of spatial and temporal changes in spawning patterns and the corresponding resulting survival of the offspring from spawning until the 1-age group. The offspring survival analysis accounts for several factors, as temperature dependent development and stage-dependent mortality, larvae feeding, whether juveniles enter the nursery grounds in the Barents Sea and size-dependent survival through the first winter. Modelled spawning intensity is systematically shifted in space and time to investigate consequences for annual survival. We find that survival is 1.52 times higher for scenarios when spawning is shifted southwards as compared to northerly shifts. In general, survival is more dependent on shifts in spawning location than spawning time. Early spawning is only favourable if spawning is concurrently shifted farther north. A future spawning scenario with a northward shift in spawning grounds beyond what has been observed historically is negative for offspring survival and, also suggests increased sensitivity to the timing of spawning.

S3O1 How do climate change and connectivity drive coral reef fish abundance in the Western Indian Ocean?

Authors: Laura Maria Warmuth[1], Michael Bonsall, Catherine Head[1,2], Melita Samoilys[3], Stephen Kelly[4], Ekaterina Popova[4]

[1]University of Oxford
[2]Zoological Society of London
[3]Coastal Oceans Research and Development - Indian Ocean
[4]NOC, Southampton

Abstract

Coral reefs worldwide are facing more risks than ever before and the Western Indian Ocean (WIO) harbours about 16% of the global coral reefs with highly reef-dependent communities. Coastal protection and food security depend on efficient conservation management, which requires understanding of connectivity and prediction of fish abundance. We aimed to explore how functional fish groups are impacted by their environment and if they respond differently to climate change stressors and connectivity. We created models for the trophic groups “grazers and detritivores”, “large excavators and bioeroders” and “corallivores” across 53 sites in the WIO. This is the first study to combine ecological models with oceanographic connectivity between coral reefs in this region. We show that different metrics of connectivity and chlorophyll a seem to be more important than sea surface temperature for all three groups. Our oceanographic connectivity metric based on particle tracking was the most important predictor for abundance of grazers and detritivores – a group highly important for reef resilience by feeding on algal turf and limiting the number of algae. Interestingly, their abundance peaked at low and high levels of connectivity which indicates that sites with a low or high particle inflow host higher grazer and detritivore numbers compared to sites with medium inflow. Results for bioeroders show abundance strongly increasing with higher chlorophyll a variability which supports that fish species have adapted to seasonal changes of alongshore currents in the WIO. Corallivores are less impacted by connectivity due to their shorter pelagic larval duration and smaller home ranges. Given the limited inclusion of connectivity into marine protected area planning, we suggest decision making must be collaborative across country borders and connectivity metrics should be used for prioritising areas for conservation.

S3O2 Timing is key: Spatio-temporal variability in mussel connectivity patterns between Marine Protected Areas in an upwelling system.

Authors: Peteiro L.G.[1], Gomes I[2], Albuquerque R.[3], Nolasco R.[3], Dubert J.[3], Swearer S.[4], Queiroga H.[3]

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[4] School of BioSciences, University of Melbourne, Australia

Abstract

Understanding spatial and temporal variability in connectivity patterns between marine populations, in order to develop efficient spatial management strategies, is still a challenge. Distinctive geochemical signatures on calcified structures according to water characteristics are increasingly being implemented as a natural tagging technique which allows a direct measurement of connectivity. We used the mussel *Mytilus galloprovincialis* as a model-species to investigate the spatial-temporal variability of the connectivity patterns among two Portuguese Marine Protected Areas (Berlengas and Arrábida MPAs) along the central Portuguese west coast. By investigating the microchemistry of bivalve larval shells (using laser ablation inductively coupled plasma mass spectrometry-LA-ICPMS) during the peaks of the reproductive season of mussels (Spring and Autumn) we generated a reference map of location-specific chemical signatures for each season. These atlases were then employed to back trace natal origins of newly settled mussels and build connectivity matrices between populations. Our results show high seasonal variability in the signals for each region, which reflects the variability of the water characteristics over the year. Nonetheless, both Spring and Autumn signals allow us to identify 3 regions with distinctive signatures: Estremadura (including Berlengas), Baía de Cascais and Arrábida. Linear discriminant analyses allowed for a high reclassification success (60%-83% and 71-82% of jackknifed cross-validated cases correctly classified in June and September respectively) based on 9 of the 16 trace-elements analyzed. The connectivity matrices allowed the identification of different pathways for mussel larvae depending on season, showing a southward prevailing dispersion pattern during spring and a reversed dispersion pattern during autumn. The seasonal variation of the connectivity patterns seems to be related to the prevalence and intensity of upwelling/downwelling episodes during each season. Since the upwelling regime is seasonal, phenological changes on reproduction might also alter the connectivity patterns between these two MPAs, and compromise the persistence of certain subpopulations.

S3O4 Understanding spatio-seasonal changes in commercial marine species through climate connectivity patterns

Authors: Marina Sanz-Martín*[1]; Konstancja Woźniacka[2]; Marta Albo-Puigserver[1]; Lucía López-López[3]; Isaac Brito-Morales[4,5]; Julia Polo[3]; Joan Moranta[1], Antonio Punzón[3], Sandra Mallol[1] and José Manuel Hidalgo[1]

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[5]Marine Science Institute, University of California Santa Barbara, USA
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Abstract

Redistribution of species that track areas with optimal climate conditions is a common strategy of marine species to cope with warming. However, the ability of species to escape unfavourable climate change local scenarios highly depends on the length of the paths they have to follow to reach better climates, which is constrained by their life-history traits and temperature preferences. Climate connectivity can be evaluated using trajectories of climate velocity – the speed and direction that a population would have to move to maintain consistent conditions. The speed of changes in species abundance and density has also been named biotic velocity. Using climate velocity and its trajectories as a metric of potential range shifts (1987-2021) and sea surface connectivity, we explore the seasonal shifts in fisheries landings (2007-2021), temperature preferences and life-history traits influence the distribution of commercial species in the Western Mediterranean Sea. We found spatial and seasonal differences in climate velocities, in length and density of paths and in the classification of climatic areas (i.e., novel and vulnerable climate areas, climate refugia and climate corridors). The most captured commercial species exhibit a strong relationship with seasonal climate velocity and climate trajectories, both variables playing a key role in the abundance of the species. Seasonal shifts in landings also differ in relation to community temperature preferences and life-history traits. Our results suggest that climate velocity and its trajectories are a useful metric to assess how climate connectivity influences recent changes in seasonal dynamics of commercial marine species across a geographic gradient in the Western Mediterranean Sea. Our approach will help identify unknown climatic risks at seasonal scale and advance towards a climate-smart management of Mediterranean fisheries.

S3O5: Impact of climate variability on the use of an estuary as a nursery habitat for flatfish species.

Authors: Ana Lígia Primo, Milene Guerreiro, Miguel Pardal, Filipe Martinho

Centre for Functional Ecology - Science for People & the Planet (CFE), Coimbra, Portugal.

Abstract

Migrations between coastal and estuarine nursery areas are essential for the successful completion of the life cycle of several marine fish. Climate change will lead to an increase in temperature and an occurrence of extreme droughts and floods in the 21st century. Coastal and estuarine systems are highly sensitive to climate extremes and changing precipitation patterns likely affecting their nursery role as well as habitat connectivity. This study evaluates the impact of climate variability on the use of a small temperate estuary (Mondego estuary, Portugal) as a nursery habitat for several flatfish species. Data from both larval and juvenile monthly spatial distribution in the estuary were analyzed during four consecutive, yet climatic distinct, years (2012-2015). *Platichthys flesus, Solea solea*, and *Solea senegalensis* early life cycle in the estuary were investigated during drought (2012, 2015) and wet conditions (2013, 2014). *S. senegalensis* larvae were present in all seasons but presented low successful settlement in the estuary. Conversely, *P. flesus* and *S. solea* were mainly present as juveniles. *S. senegalensis* larvae density was higher in wet conditions while *S. solea* juvenile was higher in dry conditions at upstream areas. Both larvae and juvenile abundances seemed not to be affected by the extreme conditions in the estuary, however, phenological changes occurred with juveniles entering the estuary earlier during dry conditions. Estuarine salinity was the main environmental factor affecting flatfish seasonal and spatial distribution in both periods. The importance of the Mondego estuary for the flatfishes species differed but played an important role during the first year for all species.

S3O6 Are jellyfish adding to the human impacts on Portuguese coastal ecosystems?

Authors: Antonina dos Santos[1,2], Rita F. T. Pires[1,2]

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Abstract

Climate change and human activities cause instability in marine ecosystems, thereby promoting species with rapid turnover, such as jellyfish. Growing evidence shows that jellyfish blooms have increased worldwide, especially in the Mediterranean Sea, leading to a wide range of impacts on ecosystems, together with multiple effects of fisheries and other human activities. In the Portuguese coast, high abundances of jellyfish may contribute to important reductions of zooplankton biomass, with potential negative effects on fish abundance and meroplankton species in general. However, until recently, there were no studies on jellyfish abundance and no knowledge about their occurrence and distribution patterns in Portugal. Therefore, the launching of the citizen science program GelAvista in February 2016, with the purpose of monitoring jellyfish populations in the Portuguese coast, provided the first information on their diversity, distribution, abundance, and seasonality in Portugal. Seven years and more than 15000 records later, we have collected information on more than 40 jellyfish species among cnidarians, ctenophores and thaliaceans, with *Physalia physalis* and *Catostylus tagi* emerging as the most sighted and abundant species. Results provided some clues on linking climate change with jellyfish dynamics in Portuguese coastal ecosystems and the possible cumulative impacts with human activities.

S3O7 Connectivity between coastal areas and estuaries for fish early life stages – a functional approach

Authors: Milene A. Guerreiro; Filipe Martinho; Manuel Rodrigues; Filipe Costa; Miguel Pardal; Ana Lígia Primo.

Centre for Functional Ecology - Science for People & the Planet (CFE), Coimbra, Portugal.

Abstract

Coastal and estuarine areas are among the most valuable ecosystems on earth, serving as nursery grounds for many species. For some fishes, both ecosystems are important considering their complex life cycles and migrations throughout development. However, anthropogenic pressures such as climate change have been imposing changes on ecosystems, altering biodiversity patterns, functional connectivity and ecosystem functioning. Studies focused on ichthyoplankton are a relatively cost-effective and efficient way to monitor fish communities and provide information on the environmental requirements of species. In this study, we analyse the fish larval communities of the Mondego estuary and its adjacent coastal zone (Portugal, North-East Atlantic) over one year (Spring, Summer, and Winter, 2021/2022) from a functional perspective. The goal is to understand the spatial and temporal patterns of trait composition and their relationship with the environment during fish early life stages in both interlinked estuarine and coastal ecosystems. For this, we considered functional and ecological traits such as use of habitat, vertical distribution, feeding type, geographical range, and egg type. Results suggest that fish larvae communities of coastal and estuarine areas can be separated into groups with differential ecological role. The estuarine environment was characterized by demersal resident, zoobenthivore and temperate species that lay demersal eggs. In turn, the coastal area hosts mainly pelagic marine, zooplanktonic species, with a subtropical distribution and pelagic eggs. Marine migrants were more abundant within the estuary, supporting it role as a nursery for species with complex life cycles. Temperature and salinity were the key environmental factors related with fish traits between systems, highlighting also seasonal differences in habitat use. This work provides important information for monitoring future changes in ecosystem functioning and connectivity, and we advocate for the inclusion of estuaries in long-term monitoring programmes to integrate the ecological processes and connectivity over fish life cycles.

S3O8 Assessing connectivity in an invasive exotic species: High reproductive potential and seasonal dynamics of early life stages of the *Alpheus* cf. *lobidens* at the southernmost coast of Europe (Cadiz Bay)

Authors: Manuel Jesús León-Cobo[1], Juan Ignacio González-Gordillo[2,3], Gustavo Freire de Carvalho-Souza[1,4], Gala González-González[1], Jose A. Cuesta[1] and Enrique González-Ortegón[1]

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Abstract

Biological invasions are a serious threat to the ecosystems, being considered one of the main causes of species extinction by exerting an extremely high pressure upon ecosystems functionality. Non-native species with a high reproductive potential and number of larval stages have a high capacity for colonize new habitats and compete with native species. The snapping shrimp *Alpheus* cf. *lobidens* is an exotic species with an invasive character recently found in the Cadiz Bay, probably arriving in Europe due to the transport of the larvae in the ballast waters of merchant ships. Until now, its potential reproductive and its number of larval stages is unknown and do not allow to model the connectivity to other regions. In this study larval population dynamic of this snapping shrimp is analyzed, focusing on how reproductive activity can benefit its dispersion via larval release. Monthly samplings have been carried out for 1 year (between 2021 and 2022), to study the larval density data in the water column, the reproductive period and fecundity. As a result, it was obtained that, number of eggs was positively correlated with female body length and ovigerous females are found all year. Higher percentage of females with eggs occurred in summer and spring, and the largest average size of ovigerous female mainly in the latest, when larvae reached in the area the highest density. Thus, although the connectivity of this species will be studied in a next step, these data showed a high reproductive potential compared to native species, and probably a better dispersal capacity, during summer and mainly in spring when more larvae were found in the study area. Additionally, during this study special attention has been paid to the identification of its unknown larval stages since this information is essential to know its dispersion capacity.

S3O9 Assessing inter-annual variability of larval replenishment and spill-over of Port-Cros National Park

Authors: Marine Di Stefano, Vincent Rossi, David Nerini

Mediterranean Institute of Oceanography

Abstract

Due to their dispersive properties and their elevated sensitivity to environmental factors, early-life stages play a key role in the spatio-temporal dynamics of marine populations. Moreover, well-enforced marine reserves provide the ideal conditions for juveniles to grow into mature adults and host larger fish with higher reproductive outputs than unprotected areas. Yet, upstream replenishing regions as well as downstream areas benefiting from the spill-over effect are poorly known, as are the environmental factors (currents, temperature, chlorophyll-a) controlling their variability. Focusing on Port-Cros National Park, we first aim at delineating the distant larval sources replenishing the reserve, and secondly, at assessing the spatial extent of the spill-over effect. Extracting dispersal traits (e.g. pelagic larval duration, spawning phenology) from a database of in-situ observations, we focus on *Diplodus sargus*, a key species of Mediterranean ecosystems and fisheries. Historical (1995, 1996, 1997, 1999) and recent (2009, 2014, 2015, 2019) data reveals significant inter-annual differences in spawning phenology and recruitment, which led us to understand the involved environmental factors and their consequences on the reserve replenishment and spill-over. Using a Lagrangian model tuned with observations, we map the dispersal pathways of fish larvae to and from Port-Cros National Park to assess the spatial extent of larval sources and sinks (and their variability due to currents). Then, the oceanographic factors (temperature, chlorophyll-a) occurring along those routes will be analysed and objectively clustered to associate a range of environmental conditions faced by dispersing larvae with specific mortality rates. Finally, the link between larval pathways, environmental conditions and mortality rates highlighted here could help Port-Cros National Park in coordinating with other downstream Marine Protected Areas during high spill-over years, or in adapting management measures during favourable replenishment years.

S3O10 Examining marine connectivity in the Strait of Gibraltar: Biophysical modelling as a tool to understand the impact of climate change on pelagic communities

Authors: Rita F. T. Pires[1,2], Peliz Á[3], Dos Santos A[1,2]

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[2] CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, Matosinhos, Portugal
[3] Instituto Dom Luiz, Lisboa, Portugal

Abstract

The Strait of Gibraltar (SoG), and the adjacent Gulf of Cadiz and western Portuguese coast, mark the transition between distinct systems in the northeastern Atlantic, harbouring a mixture of temperate, tropical and boreal species. The area is extremely interesting in what regards marine connectivity and the transport of pelagic larval stages. Understanding species transport in the area is paramount for the management of over- exploited populations, and to minimize the impacts of climate changes in the oceanic features and, ultimately, the biological communities. As a major route for commercial ships, the human-induced impacts are inevitable. Biophysical modelling exercises are presented, combining oceanic and particle-tracking Lagrangian simulations with *in situ* spatial and vertical plankton data collected in the area. The conditions driving the exchange larvae between sub-basins and the connectivity throughout the region were explored, using crustacean decapod larvae as biological references. Results suggest that species transport and distribution are influenced not only by the complex local topography and ocean circulation, but also by the particular environmental conditions found in each side of the SoG. The simulations showed that larvae are contrastingly favoured when crossing the SoG, according to their spawning grounds, larval duration and vertical migrations, impacting the effective larval input into the Atlantic or Mediterranean sub- basins. Scenarios of climate change and human-induced activities will be discussed: alteration of dispersal pathways caused by shifts in the circulation patterns; changes in spawning grounds or larval duration prompted by temperature and salinity changes; and the introduction of species. The study shows how enhanced knowledge on how temporal and spatial variability impact larval dispersal may allow improved biodiversity assessments and conservation measures, and help to understand the conditions favouring the introduction of new species.

S3O11 Direct human-induced alteration of the timing of environmental seasonal events - oceanic fish farm in Israel as a case study.

Authors: Ziv Zemah-Shamir*, Dan Tchernov, Aviad Schinin

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Abstract

The rapid growth of the human population is one of the main causes of the huge global ocean changes, that we are facing today. This population increase also creates a numerous demand for food which leads to overexploitation of ocean resources, like overfishing, impacts a great number of species worldwide, and causes environmental degradation. Due to extensive and expanding overfishing of wild-caught seafood and ocean fish farming has grown to augment the supply of fresh fish to the food markets. Ocean fish farming becomes one of the fastest-growing global industries today. Ocean fish farming appears to aggregate multiple species of sharks that become permanent residents for long periods. The shores of the Mediterranean Sea are dotted with such fish farms, which are attractive areas for a variety of marine predators, including several species of sharks. In the south of Israel, a fish farm was established to breed bream fish in the deep sea (bottom depth 70 meters). The research objective is to monitor and understand the reasons for the grouping of sharks at different times of the farm's operations. in order to understand the reasons, we are carrying out long-term monitoring. our main results show that the factor explaining the presence of the sharks was in perfect correlation with the mortality of sea bream fry on the farm. Our concern was that the availability of food near the coast might delay shark migration, change behavior patterns, and create dependence on this anthropogenic disturbance.

S3P1 Sharks and rays growth and interactions with the commercial fisheries in South-eastern Adriatic Sea (Albania)

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Abstract

Because of their life history characteristics, sharks and rays appear to be particularly vulnerable to several threats where overfishing is considered the most important. In presented study four shark species and three rays were sampled from the catches of the commercial fishing vessels. Based on available sample size, length weight relationships were estimated for two sharks (common smooth-hound and longnose spurdog) and two rays (Mediterranean starry ray and thornback ray). A linear regression analysis performed on log-transformed data was used to estimate intercept and slope, and to describe the length–weight relationship for each species. Following this regression, parameter b ranged between 2.4-2.7 indicating a negative algometric growth of these species. These are considered to play a key role in marine communities and thus the study and management of their populations should get a particular attention in the frame of implementing ecosystem-based approach of biodiversity.

S3P2 Susceptibility to climate change of different taxa through latitude.

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Abstract

Thermal tolerance range greatly vary throughout the world being directly interconnected with the different habitat's temperature variation. Tropical animals are usually subjected to higher environmental temperatures, however several studies have suggested that these are the animals more susceptible to climate change when compared to other regions. One of the most common methods used to assess a populations' thermal tolerance is Critical thermal maxima (CTMax). In the present work I collected data from many studies using CTMax information to infer thermal tolerance of different species populations throughout the world and compared it with latitude as a proxy of the climate each species live. Also, for each climate, the difference in thermal tolerance was analyzed between taxonomic classes. The CTMax value clearly increases from the poles to the equator as it would be expected but presenting a high value also in the temperate region. The difference between the CTMax and the environmental temperature (Thermal safety margins - TSM) follows an opposite trend with the tropical species being the ones more susceptible to climate change. However, as in the CTMax, there is a peak in the TSM values for the temperate species. Mollusks, in special bivalves presented higher CTMax and TSM values. Such trend was mainly seen in the temperate region in which these taxa are exposed to high temperatures in the intertidal areas.

Theme session 4 - Critical connectivity hubs and pathways at sea and the land-sea interface

23 May 2023 -24 May 2023

Conveners:
Anna M. Sturrock, University of Essex, United Kingdom
Maria Beger, University of Leeds, United Kingdom

Connectivity is defined by the flux of organisms across habitat patches and underpins ecological functions. Understanding the key hubs and pathways linking patches is critical to quantifying marine functional connectivity and implementing effective resource management. Importantly, humans have disrupted natural connectivity. Climate change, habitat fragmentation and spatially explicit stressors, such as shipping and fisheries, can reduce flows, but they can also modify pathways and create new ones, promoting the spread of invasive species.

This session calls for studies assessing the role of critical habitats and pathways, physical structures, animal movement, individual behavior etc. on supporting and/or modifying connectivity, and how such knowledge can inform actions to preserve and manage it.

S4 Keynote: The impacts of extreme drought on salmon connectivity across the land-sea interface

Keynote: Anna M. Sturrock

Authors: Anna M. Sturrock[1], Flora Cordoleani[2], Malte Willmes[2], Corey C. Phillis[3], Stephanie M. Carlson[4], William H. Satterthwaite[5], Eric Huber[6], Carson Jeffres[7], Rachel C. Johnson[5,7]

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Abstract

The complex salmon lifecycle creates important cross-ecosystem linkages across the land-sea interface, bringing marine subsidies far inland and replenishing large ocean fisheries. California is at the southern edge of the Chinook salmon native range, and its populations are struggling due to habitat loss and degradation, and increasingly extreme droughts. Here, we showcase three studies exploring how human actions, both past and present, are interacting with droughts to influence the connectivity and resilience of Californian salmon populations, demonstrating how decisions made far upstream can significantly influences processes in the ocean. 1. Habitat loss. The loss of cooler, high elevation habitats means that most juvenile salmon in California can no longer survive a summer in freshwater, and thus the late-migrating strategy is now rare. In two of the last remaining undammed rivers, we used otolith reconstructions to show that - by avoiding the warm low elevation migratory corridor in spring/summer - these slow growing, late migrants have a selective advantage during droughts, providing important climate resilience. 2. Dam management. Using juvenile salmon abundance data, we show that water capture behind dams during winter can suppress important migratory cues and delay salmon emigration, increasing in-river mortality and reducing land-sea connectivity. The truncation of phenological diversity further increases risk of cohort failure via match-mismatch dynamics, given that ocean upwelling timing is particularly variable in this region. 3. Hatchery supplementation. The high mortality rates of salmon across the freshwater landscape during droughts has prompted an extensive 'trucking program' where hatcheries transport millions of smolts directly to the estuary during droughts. We analysed historical release records and mark-recapture tagging data to explore the evolution of this practice and its consequences; with straying rates of trucked salmon often an order of magnitude higher than on-site releases, resulting in genetic and demographic homogenization and a weakened portfolio effect.

S4O1 The origin, dispersal pathway, and connectivity of invasive lionfish Pterois miles in the Mediterranean

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Abstract

The widespread invasion of lionfish *Pterois miles* in the eastern Mediterranean and the western Atlantic Ocean has revealed that it is a successful invader and can have destructive effects on native species, having indirect ecological outcomes and economic effects on regional fisheries, truism, and human health. In the present study, mtDNA COI, Cyt b, and 16S rRNA genes of lionfish from Turkish marine waters as well as sequence data from the whole distribution of the species including the Mediterranean, Atlantic Ocean, and Pacific Ocean were analyzed to reveal the origin, dispersal pathway, colonization and bottleneck effect, and connectivity of lionfish. DNA sequences of mtDNA COI, 16S rRNA and Cyt b gene regions were scanned in the Genbank Standard Nucleotide BLAST database, and the accuracy of the sequences was approximately 98% to 100% similar to only *Pterois miles* samples reported from the Mediterranean, Red Sea, Javanese Sea and Indian Ocean. Genetic analyses of the Mediterranean and Aegean populations of lionfish indicate that different haplotypes play an important role in the success of spreading and invasion as one goes from east to west and north. The invasive *P. miles* populations in the Mediterranean were genetically related to the Red Sea, which is the natural distribution area of the species. Different haplotypes have been successful in spreading and invading, creating a Founder effect in both the Red Sea and the Mediterranean. Moreover, lionfish populations in the Red Sea are not genetically related to the populations of the Pacific Ocean. On the other hand, lionfish in the Mediterranean have no connection with the lionfish in the Atlantic Ocean.

S4O2 Combining acoustic telemetry and stable isotope analysis to improve *Raja undulata* connectivity patterns

Authors: Paula Daban Losada[1], Alina Hillinger[2], David Villegas-Ríos[3], Gonzalo Mucientes[3], Andreu Blanco[4], Alexandre Alonso-Fernández[3]

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Abstract

Understanding functional connectivity of threatened species must provide critical information for an effective management and conservation spatial planning. In this study, we use a non-lethal novel combination of acoustic telemetry and stable isotope analysis (SIA) on a “Near threatened” elasmobranch, *Raja undulata*, to test that the isotopic niche width is dependent of behavioural patterns in relation to the space use within a marine protected area. Acoustic telemetry records of a local population of *R. undulata* within waters of a national park in NW Spain revealed a seasonal aggregation during summer. Yet, our results also evidenced that up to 32.65% of the studied individuals can be classified as resident based on their residency patterns. Resident skates showed narrower isotopic niche width than seasonal summer visitors, as these individuals were likely exposed to a limited variety of habitats and resources. Conversely, seasonal visitors showed wider isotopic niche widths, where females have larger isotopic niches, indicative of greater diversity of resources use from different environments. Therefore, we hypothesize that seasonal visitors play an important role connecting different habitats, and even populations, along the coast particularly through dispersing patterns of females. This study provides valuable insights into the spatial and resource ecology of *Raja undulata* and their role in the functional connectivity of the coastal ecosystem, key information for the management of marine protected areas.

S4O3 Coastal connectivity of an abundant inshore fish species, model-data comparison along the south coast of South Africa

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Abstract

Biophysical models are often used to estimate larval dispersal patterns for the assessment of marine metapopulation spatial structure. Comparisons of these models with field observations are however relatively rare, and the extent to which models reproduce true marine connectivity patterns is unclear. We developed a biophysical model for larvae of the blacktail seabream (Sparidae: *Diplodus capensis*), an abundant recreational and subsistence fishery species along the south-east coast of South Africa and compared outputs from various configurations of that model to results from a field study conducted in a large regional embayment. Seasonal patterns of dispersal and recruitment produced by the model agreed best with field observations when thermal constraints on spawners and larvae were included. Spatial gradients in settling larvae also matched well, with the model capturing observed high settler densities within the lee of a major headland. Nevertheless, stronger spatial gradients were observed in larval densities from the field study when compared with model results, which may be explained by behavioural post-settlement processes. Model-based dispersal patterns revealed up to five subpopulations along the southern coast with barriers to connectivity between subpopulations generally linked to hydrographic features. Overall, our results suggest that thermally-mediated spawning behaviour, physical transport and post-settlement processes all play important roles in determining marine connectivity for the blacktail seabream. Even so, our study indicates that even relatively simple biophysical models can provide useful information on connectivity and potential population structure which may be used to inform spatial area management of exploited fisheries.

S4O4 Connecting population functionality with distribution models predictions to support freshwater and marine management of diadromous species

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Abstract

Diadromous species have a complex life cycle during which they migrate between marine and freshwater habitats. They experience multiple human-induced pressures in both environments, often exacerbated by climate change, leading to dramatic population declines across their distribution ranges. Given their poor conservation status, present and forecast distribution models have been implemented separately in both environments to improve understanding of their conservation status. However, habitats connectivity has not been analysed. Here, a single framework is proposed, linking marine and freshwater Species Distribution Models (SDM) outputs with current observations of population functionality to study the ecological connectivity between both ecosystems. The potential effects of climate change are also included through future SDM projections to guide more integrative and long-term management. A decision tree was developed and applied to about hundred catchments in the study area from southern Portugal to southern Scandinavia for two anadromous species (*Alosa alosa* and *A. fallax*; reproducing in rivers) and two catadromous species (*Platichthys flesus* and *Chelon ramada*; reproducing at sea). Their current population status was assessed from the EuroDiad 4.0 database and compared with current and future catchment suitability assessments (from the hybrid SDM, HyDiaD). Connectivity between the abundance assessments and distribution models were then matched with current and future hierarchical distribution models of diadromous fish at sea to inform population viability. Finally, with the help of national diadromous species experts, we focused on four catchments distributed along the European latitudinal gradient to test the proposed methodology and highlight local management challenges in terms of land-sea continuity and environmental quality.

S4O5 Identifying critical habitat patches and connectivity pathways in the Northwest Atlantic Ocean; using particle tracking and graph theory to understand connectivity in a habitat forming deep-water coral

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Dalhousie University

Abstract

The dispersal of marine organisms across seascapes is a key process in maintaining biodiversity and population persistence. Patterns of larval dispersal and connectivity within a spatially fragmented population can be used in combination with graph theory metrics to identify critical habitat patches for the persistence of a metapopulation. Here, we used a 3-D Lagrangian particle tracking model coupled with an ocean circulation numerical model to simulate larval dispersal for the habitat forming deep-water coral, *Lophelia pertusa*, in the Northwest Atlantic Ocean. Larvae were released each month from January 2005 to December 2019 and tracked for 60 days, which is the estimated Pelagic Larval Duration for *L. pertusa*. Using these tracks, we identified habitat patches critical for the overall connectivity of *L. pertusa* in the region. Strong seasonal and interannual variability in connectivity among habitat patches suggest the timing and duration of spawning will greatly affect connectivity between populations, variables which are currently unknown for NW Atlantic populations. Results also show that the length of the pre-competency period greatly influences the strength and number of connections across populations. We calculate closeness centrality, eigenvector centrality, and directionality for current and future climate scenarios, when suitable habitat is predicted to decline due to acidification, deoxygenation, and decreased food availability. Our results can help to inform which populations of *L. pertusa* in the NW Atlantic should be prioritized for climate-smart protection and preservation to optimize the resilience of the network.

S4O6 Circumpolar population structure and connectivity of polar cod (*Boreogadus saida*)

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Abstract

The Arctic Ocean is experiencing rapid environmental changes, including alterations in sea-ice conditions that have a direct impact on the organisms living in close association with sea ice. One of those organisms is the polar cod (*Boreogadus saida*), an abundant fish with circumpolar distribution and a key species in the Arctic marine food web. Despite its ecological importance, the spatial genetic population structure and connectivity are not fully understood. We used 812 high-quality single nucleotide polymorphisms (SNPs) obtained through genotyping-by-sequencing to assess the circumpolar population structure as well as local and large-scale connectivity patterns. At a circumpolar scale, four large-scale groups are genetically differentiated at a low, but significant level (F_{ST} ranging from 0 - 0.108): *Alaskan Arctic* (Beaufort and Chukchi Sea), *Transpolar Drift* (Iceland, Laptev Sea, Northeast Canada) and *Europe* (Central Arctic Ocean, Svalbard, Northeast Greenland and West Greenland) with sub-structuring detected in all these groups. Furthermore, at least two individuals (one collected in Northeast Greenland and one in the Laptev Sea) constitute a fourth genetically differentiated group. Connectivity driven by sea-ice drift associated dispersal of larvae and juveniles, as well as active migration by adults via warm Atlantic water and coastal currents, and the potential presence of different ecotypes with intrinsic behavioural mechanisms for migration and spawning might explain genetic differentiation patterns. Future disruptions in sea-ice pathways due to climate change will likely act as a barrier to gene flow and hamper connectivity of sea-ice associated larvae and juveniles. While adult dispersal may be less affected, ongoing loss of spawning habitat is likely contracting the distribution range and biomass. It will be important to monitor the evolution of the polar cod metapopulation in the future.

S4O7 Anthropogenic threats on the 3 dimensions of shad populations connectivity: marine connectivity, land to sea connectivity, and connectivity between shad populations

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Abstract

Anthropogenic threats on the 3 dimensions of shad populations connectivity: marine connectivity, land to sea connectivity, and connectivity between shad populations. Like other anadromous species, Shads *Alosa alosa* and *Alosa fallax* reproduce in river headwaters, migrate to marine habitats to complete their growth and sexual maturity before returning to their spawning grounds. Shads express alternative reproductive strategies, reproducing either in their natal river (homing) or in a different river (straying). Straying induces a significant exchanges of spawners between shad populations, implying the use of connectivity across marine habitats. Overall, we have identified three levels of habitat connectivity that are key issues for shads: the river to sea continuum, the connectivity within the marine habitats, and the connectivity between populations. Within the Diades INTERREG project, we have collectively addressed how anthropogenic pressures impacted these three levels of connectivity in shads using case studies. An approach based on otolith natal fingerprints was used in different European contexts to track shad natal origin, in order to infer individuals movements between natal site and sampling site. Land to sea connectivity was studied in the context of restoration of Mondego and Garonne Rivers. The interaction between fisheries and marine habitats use was investigated using the otolith-based natal origin tracking of shads sampled as bycatch in marine habitats of the North Eastern Iberian Peninsula. Lastly the study of the level of exchange of shad spawners between different shad populations in rivers of Southern Ireland, Southern UK and Northern France was undertaken by sampling spawners on river sites and adults at sea. Results confirmed the essential role of habitat connectivity at all stage of their life cycle. The three case studies provided evidence of the interplay between social behavior, relative demography of shad populations, and interspecific differences between *A. alosa* and *A. fallax*.

S4O8 Otolith chemistry suggests multiple origins of northern range-expanding gilthead seabream populations.

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Abstract

To sustainably manage range-expanding, exploited marine resources in the face of ongoing global change, a thorough understanding of the connectivity processes underpinning species resilience to environmental change, and population source-sink dynamics, are required. As an example, the gilthead seabream *Sparus aurata* is a high value sparid fish currently undergoing a poleward range shift in response to warming sea temperatures. Northern stocks of *S. aurata* have recently become established in the English Channel and Celtic Sea. Knowledge of *S. aurata* population structure in the north-east Atlantic is limited, however recent research suggests genetic differentiation between the new northern stocks and those located further south. This outcome is likely dependent on local adaptation having facilitated the successful breeding of more thermally tolerant individuals in cooler northern waters. Drawing on multiple cohorts of *S. aurata* sampled from two nursery sites located 200 km apart along the southern UK coast, we tested multi-elemental otolith fingerprints from early larval life to investigate the spawning origins of these northern fish. The data revealed three distinct spawning origins with significantly different signatures in Sr, Mg, P and Mn, irrespective of the cohort sampled. The contribution of the three spawning origins to each nursery site varied, and further suggested mixed spawning origin at both sampled sites. Although part of this mixing could occur during juvenile or sub-adult movement, these data suggest that larval recruitment may be occurring at higher latitudes than has previously been reported. Our results suggest that fisheries management at the frontiers of range-expanding species may require broader consideration of connectivity at a level appropriate to protecting source populations.

S4O9 FRESHseaBASS - Divergent sea bass freshwater incursions

Authors: Almeida R.[1], Mateus C. S.[2], Tanner S. E.[1,3], Ribeiro F. [1] & Quintella B. R.[1,3]

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Abstract

The European sea bass (*Dicentrarchus labrax* (Linnaeus, 1758)) is a highly valuable marine species targeted by commercial and recreational fisheries. The species is euryhaline and considered a partial migrant due to the co-existence of distinct migratory phenotypes. Both long-distance migrations towards wintering grounds and residency behavior in coastal habitats have been observed in sea bass. Juveniles make extensive use of estuaries and may even occur in freshwater environments, whereas this behavior was only recently detected for adults. Sea bass captured by fishermen, approximately 150km upstream of the Tagus River mouth (Portugal), during 2021-2022, were analyzed to characterize the species' freshwater contingent structure. Complementarily, to identify patterns and potential changes in the sea bass freshwater habitat use, questionnaire surveys with fishermen were conducted. The results showed that not only juveniles but also adults occur in freshwater habitats, with the captured individuals ranging between 28.5cm-59.7cm in total length and 223g-1837g in total weight. Both males and females were observed in the adults detected in freshwater (1:1.7 Male-to-Female ratio). Although occasional catches are reported throughout the entire year, most individuals are caught in September-October, aggregating immediately downstream of the first barrier of the Tagus river (Abrantes weir). While no individuals were recently caught upstream of this weir, fishermen reported the occurrence of the species in upstream areas prior to the weir's construction (2004). The occurrence of European sea bass in freshwater environments reinforces the need to preserve longitudinal connectivity, not only for diadromous and potamodromous species but also for marine migratory species with freshwater contingents. Different migratory phenotypes may increase species' resilience against multiple pressures, thus it is key to consider these different phenotypes to ensure effective conservation and management efforts. Works are ongoing to unravel sea bass freshwater migrations and to assess the relative importance of the freshwater contingent in this population

S4O10 Seascape connectivity modelling predicts potential hotspots of fish-derived nutrient provisioning to restored coral reefs.

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Abstract

Coastal habitat quality and quantity have been significantly eroded by stressors operating and interacting across the land-sea interface, prompting a recent proliferation in coastal restoration programs worldwide. These initiatives often recognize connectivity as a critical driver of ecosystem functioning, yet few include connectivity as a spatially explicit, quantitative criterion during the planning process. Here, we demonstrate the use of spatial graph models to quantify potential functional connectivity for two multi-habitat-utilizing reef fish species known to transport nutrients and other ecological functions from nearshore mangrove and seagrass nurseries to oligotrophic offshore reefs. Applying the method across sites considered by a multi-million dollar coral restoration program in the Florida Keys, USA revealed locations where outplanted corals are likely to benefit the most from enhanced functional connectivity in the form of nutrient provisioning by reef fishes. Opportunities for positive interactions varied between fish species, owing to selective patterns of habitat use, and highlight the need for species-specific connectivity assessments, even within a trophic guild. Connectivity estimates for candidate restoration sites were influenced more strongly by habitat composition (which influences fish foraging and shelter resources) than by proximity to potential mangrove and seagrass nurseries, emphasizing the importance of considering both seascape composition and configuration in restoration design. Ecologically and economically effective restoration strategies are urgently required to curb rapid declines in coral reef architectural complexity, ecological function, and resilience. Our study illustrates the utility of spatial graphs as a data- and resource-efficient technique for quantifying and communicating complex ecological connectivity information in service of such efforts. Critically, though, models of potential functional connectivity should serve as only one component of a larger, interdisciplinary site selection framework to ensure that desired outcomes are met.

S4O11 Tracking adult meagre in the Tagus estuary: a contribute to understand the estuarine-sea interface during the spawning season.

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Abstract

The meagre is among the iconic Sciaenidae species, attaining a large size at a longevous life, and forming ephemeral spawning aggregations. This migratory marine fish has a broad geographical distribution, encompassing the Central Eastern Atlantic Ocean's and part of the Eastern Atlantic Ocean's coastal waters, including North Africa, the Mediterranean and the Dead Sea. In Portugal, the species value has been attributed mainly by its importance for artisanal and recreational fisheries, and particularly in the vicinities of the major estuaries, as the Tagus estuary, where approximately two thirds of the country catches occur. Further awareness is presented in recent studies pointing the Tagus estuary as a critical spawning and nursery area in the west coast of Portugal, with high conservation risks related to persistent target fishing. We address the adult meagre site fidelity and movements in the Tagus estuary using an acoustic biotelemetry approach. From 2019 to 2022, an array of #16 acoustic receivers were deployed receiving #XX signals from 26 meagre tagged with acoustic transmitters. We used estuarine revisits to run agent-based simulations and analyze the species site fidelity to the spawning area. Additionally, we studied the species movement behavior using network analysis to represent the seasonal and annual spatial structure of each meagre trajectory, and the aggregated specimens' dataset. Additional receiver arrays deployed in Portugal (CoastNet research infrastructure) extends the spatial scale of the study to adjacent major estuaries and coastal waters. However, no specimens were detected on relatively nearby estuaries where the species regularly occurs, thus, supporting the current breeding population unit model. Our results provide the first in-situ data of meagre movements in the Tagus estuary and highlight the functional connectivity between the estuarine habitat and the adjacent marine coastal waters. Thus, it is expected that the work can contribute for increasingly refined management plans.

S4O12 How well do existing Natura 2000 areas capture marine functional connectivity?

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Abstract

Area-based conservation measures can be highly effective conservation tools to counteract ecosystem declines arising from anthropogenic forces and climate change. However, on larger spatial scales these sites may prove insufficient and ineffective, particularly for migratory or wide-ranging species. The Natura 2000 system is the largest systematic assemblage of conservation areas in the world, currently protecting 8 % of the European Union's marine waters. However, the majority of these sites were designated with little consideration of systematic conservation planning principles, particularly with regards to connectivity. Connectivity underpins species persistence and ecosystem resilience, and thus is pivotal to the effectiveness of a system of conservation areas, yet it is currently unknown how connected the Natura 2000 system is. Here, we evaluate the marine functional connectivity of Natura 2000 sites with meta-population benefit functions for two case study areas. We collate biophysical larval dispersal data, species migration information, and genetically derived connectivity estimates to represent connectivity for species and life history types across multiple taxa (e.g., fishes, molluscs, …). Using geographical information systems (GIS) and MarxanConnect spatial planning software, we evaluate the degree of marine functional connectivity encapsulated by the Natura 2000 network and identify where priorities for additional sites are located. Our findings demonstrate that the effectiveness of Natura 2000 sites in capturing connectivity varies by region and life history (species). The degree to which the system captures marine functional connectivity largely depends on the life histories of the species examined. In sum, our results demonstrate that the Natura 2000 system is largely effective in protecting connected sites for many species, and that the management of anthropogenic activities around Europe can be adjusted.

S4O13: Modelling larval connectivity among subsea oil and gas platforms in the North Sea and the Southeast Gulf of Mexico.

Authors: C. Gabriela Mayorga Adame[1], Jame Harle[1], Nuno Simoes[2], Jeff Polton[1], Jason Holt[1], Lea-Anne Henry[3]

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[2] Universidad Nacional Autonoma de Mexico, Yucatan, Mexico
[3] Heriot-Watt University, Edinburgh, UK.

Abstract

Subsea oil and gas platforms introduce hard substrate to the marine environment. After some time the structures are colonized by hard-bottom marine organisms with platforms commonly functioning as artificial reefs. Whether they work as a network, interconnected by pelagic larvae that interact with natural reefs is an important ecological question, since these interactions can have to both positive (i.e. promote biodiversity, increase biomass) and negative impacts (i.e. facilitate the dispersal of non-native species). We use a particle tracking model couple to high-resolution regional ocean circulation models to investigate the spatial and temporal scales of connectivity among oil and gas platforms in the North Sea and the Southeast Gulf of Mexico. Network analysis is applied to the resulting connectivity matrices to identify sources and sinks, connectivity hubs, and stepping stone subsea structures. Regional differences in connectivity are expected due to the different oceanographic regimes in the different regions and the geographical distribution of the subsea structures. Larval characteristics, particularly PLD, are expected to drive differences in the connectivity patterns for different species groups.

S4P1 Cumulative and In-Combination Effects of Offshore Infrastructure on Ecological Resources.

Authors: Ellie-Mae Elizabeth Cook, Krysia Mazik, Bryony Caswell, Sue Hull, Rodney Forster

University of Hull

Abstract

Offshore wind is experiencing substantial scale-up as demand for renewable energy urgently increases to meet global 2050 net-zero targets. This has led to rapid expansion of offshore infrastructure, resulting to physical disturbances and fundamental changes in habitat type. Large amounts of new artificial hard substrata are being introduced and the nature of the surrounding seabed is being modified, causing changes in local faunal communities. In isolation these changes may have only local consequences, but the cumulative impacts and in-combination effects on ecological resources are not yet known. Significant impacts on the structure and functioning of marine ecosystems at large, landscape scales are likely. Furthermore, faunal changes both on and in the vicinity of the new infrastructure will have implications for functional connectivity. This project explores soft-sediment communities near to various types of structure, across a range of soft-sediment habitats, over different spatial scales at three sites along the Holderness coast and in the Humber estuary, UK. Eight coastal defence groynes were sampled seasonally along transects, up to 90 m either side of each structure at different tidal heights. The spatial and temporal impacts of groynes on sediments and benthic community structure and functioning, will be investigated as a proxy for future investigations of offshore wind infrastructure (e.g., cables or monopile foundations). Preliminary results suggest groynes influence both the sediment type and macrofaunal species present, with sediments close to the groynes containing twice the number of organisms and taxa groups compared to those 90 m away, on many transects. Information on structural changes will form the basis of biological traits analysis to determine changes in potential ecological functioning, including organism mobility, nutrient and energy flows. These results will be used to estimate the cumulative effects of new offshore infrastructure in the North Sea and the implications for ecological functioning and connectivity.

S4P2 Connectivity and adaptation of *Trematomus* fishes across the Antarctic continental shelf.

Authors: Marie Verheye[1]*, Henrik Christiansen[1],[2]*, Franz M. Heindler[1] , Enora Geslain[1] , Iliana Bista[3] , Agnes Dettai[4] , Bart Hellemans[1] , Anton Van de Putte[5],[6], Isa Schön[5] , Filip. A.M. Volckaert[1]

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Abstract

Polar ecosystems harbour a unique cold-adapted biodiversity that is threatened by rapid environmental change. In this context, multi-scale data on connectivity and adaptation are essential for supporting the exploitation and conservation management of living resources and ecosystems. Notably, marine protected areas (MPAs) are most effective if implemented as a network that considers functional diversity within and between species. In the present study, population genomics is used to advance our understanding of spatial connectivity in Antarctic notothenioid fishes. A total of 698 individuals of ten *Trematomus* species were genotyped using ddRAD sequencing. Thousands of single nucleotide polymorphisms (SNP) were used to investigate patterns of divergence and genetic connectivity across the Antarctic continental shelf. Genome scans for putatively adaptive loci and genotype-environment associations analyses aimed to explore potential adaptations of populations to local environmental conditions. Within *T. eulepidotus*, all individuals from the South Orkney Islands, Filchner Trough and some of the Filchner West samples are clearly differentiated from individuals sampled in other Eastern Weddell Sea areas. A similar pattern was observed in *T. loennbergii* for which Ross Sea, Western Peninsula and Filchner Trough samples are differentiated from individuals collected in other Eastern Weddell Sea areas. Altogether, these results suggest long-range dispersal across the Weddell Sea and even along the entire West Antarctic coast (for *T. loennbergii*) and a genetic break at the Filchner Trough. The Filchner Trough area is characterized by strong outflow from the Filchner-Ronne ice shelf. This outflow may separate the trough area from the remaining Weddell Sea habitat, while transport along the western coast of Antarctica might occur at a larger scale via the Weddell Sea Gyre and Antarctic Coastal current. Our results contribute to the assessment of biological variation in adaptation and connectivity in the Southern Ocean, which is imperative in view of unprecedented global change.

S4P3 Investigating the Transversal Connectivity of Coasts, Wetlands, and Freshwaters to Natural Landscapes within the Northern Mediterranean Metropolitan Areas.

Authors: Artan Hysa[1], Jürgen Geist[1], Roland Löwe[2]

[1] Aquatic Systems Biology
[2] Technical University of Denmark

Abstract

Coastal zone (CZ) is a vibrant area within the ocean-continent interface. It makes home od several conflicts between anthropogenic and natural systems. Wetlands are vital nodes in the CZ gradient. They function as biodiversity hinges for the transition between aquatic and terrestrial species, nutrients and food flows. However, the human intervention in the CZ is significant and put pressure to these unique habitats. Even though the sensitivity of the community about the conservation of these areas is promising (RAMSAR sites), their long-term prosperity depends on the connectivity they have to the terrestrial natural habitats and vice versa. In this study we argue that a healthy wetland habitat relies on well-connected network of blue-green infrastructure. We stress on the transversal connectivity rather than the longitudinal one. We advocate that the deeper the transversal connectivity the richer the biodiversity within the gradient of sea-wetland-land. We focus on the metropolitan areas along the northern Mediterranean coastal zone including hinterlands of large cities like, Barcelona, Rome, Marseille, etc. We rely on Urban Atlas (UA) LULC data derived from Copernicus database. Our method relies on transversal connectivity index (TCI) which is a GIS-based procedure developed for assessing the existing and potential transversal connectivity of natural landscapes to water surfaces. Our study shows that even though wetlands of the northern Mediterranean are protected, they are significantly disconnected to further inland natural landscapes. While. The transportation infrastructure appears to be the main fragmenting driver. Yet, reconsidering some land-uses and human infrastructure can enhance the transversal connectivity of coastal wetlands to natural landscape mosaics. Transversally well-connected wetlands to continental natural landscapes will expand the species connectivity into a marine-wetland-terrestrial gradient.

S4P4 Reintroduction of Dugongs to China by Gradually Restoring their Habitat.

Authors: Samantha Ma[1], Zhou Jinfeng

[1] China Biodiversity Conservation and Green Development Foundation (CBCGDF)

Abstract

Dugongs were once mainly found in the southern coastal waters of China, but now are extinct. The main culprit for the functional extinction of dugongs in China is the loss of their habitat due to the wanton killing of dugongs and the destruction of the offshore ecological environment. In view of the successful reintroduction of Père David's Deer, China Biodiversity Conservation and Green Development Foundation (CBCGDF) established a dugong group in 2022 and formulated a work plan for the next three years, aiming to work with the international community to reintroduce the species to China by restoring the entire ecosystem on which dugongs depend. CBCGDF originated from China Père David's Deer Foundation, which reintroduced 38 Pères David's Deer to China in 1985. As a leading ENGO in China, CBCGDF has always put biodiversity conservation at the top of its agenda. CBCGDF has developed a series of effective biodiversity conservation concepts such as "Biodiversity Conservation in Our Neighborhood (BCON)" and Human-based Solutions (HbS), and has established about 190 Community Conservation Areas (CCAfa) throughout the country, actively promoting the mainstreaming of biodiversity conservation. Biodiversity conservation, including dugongs, can be carried out in three steps: 1. protection, i.e., maintenance of the natural environment and reduction of disturbance of the marine environment by human activities; 2. restoration, i.e., natural recovery through designation of marine protected areas and rewilding; 3. conservation, i.e., targeted scientific research on offshore organisms The first step is to use scientific methods to enable organisms to flourish naturally. The most urgent task is to restore and re-establish the habitat of dugongs in the offshore, including restoring seagrass beds and setting up nature reserves, as well as re-establishing marine connectivity and forming bio-bridges, in the hope that dugongs can return to the offshore of China through migration by natural means.

S4P5 Factors influencing the success of early marine migration in Atlantic salmon and managment implications.

Authors: Colin David Bull[1], Neil Banas[2], Emma Tyldesley[2], Aislinn Borland[2]

[1] Missing Salmon Alliance
[2] University of Strathclyde

Abstract

Atlantic salmon are an important diadromous fish species experiencing population declines across their range, driven largely by reduced survival during their extended marine phase. Understanding and maintaining effective connectivity routes between essential aquatic habitats is a key focus area for current and future salmon management. The conditions experienced during the initial marine migration between freshwater rearing areas and the rich open ocean feeding grounds are recognised as a period of intense natural mortality pressure, although the actual driving mechanism are still largely unknown. Climate change induced changes in conditions are locally-exacerbated by risks posed by marine fisheries and other anthropogenic developments (e.g. offshore wind power generation) along this route. Here we present results on assessing conditions and possible mortality factors during early marine migration: 1. How fluctuations in the available energy in lower trophic levels play a vital role in governing survival during the initial outward migration of salmon from UK and Ireland rivers and 2. How novel individually-based modelling techniques can be used to predict future migration routes and identify potential bottleneck areas.

S4P6 Population discrimination of *Helicolenus dactylopterus* and *Merluccius merluccius* in the Atlantic and Mediterranean using otolith shape analysis.

Authors: Ana Vaz[1]*, Susanne Tanner[2], Milene Alexandra Guerreiro[1], Patrick Reis-Santos[3], Christoph Stransky[4] , Miguel Pardal[1] , Filipe Martinho[1]

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Abstract

The delineation of fish population structure contributes to a better understanding of connectivity patterns and to fisheries management. In this study, we used otolith shape analysis to identify population structure and connectivity along the Atlantic and Mediterranean Sea for the commercially important marine fish species *Helicolenus dactylopterus* (Blackbelly rosefish) and *Merluccius merluccius* (European hake). The shape outline reconstruction from the average of all otoliths showed a clear difference among populations in both species, as reflected by the high level of variation of the Wavelet coefficients. A clear separation between the more northern populations, the Portuguese islands and the Mediterranean Sea was found, as well as withing these groups for both *H. dactylopterus* and *M. merluccius*. In agreement, the ANOVA like permutations test showed significant differences in the otolith shape among most of the populations of each species. For the Blackbelly rosefish, samples from Norwegian Sea are clearly separated from the rest, as evidenced by the first axis of the Canonical Analysis of Principal Coordinates (CAP). However, the degree of discrimination decreased within the other two groups, the central (central and southern Portugal and Sicily) and the north group (Faroe Islands, North Sea and north Spain). In European hake, only North Sea, Sicily and Cyprus populations were clearly distinguished by the CAP, as well as a high overlap between Bay of Biscay, Portugal and southern France. This work supports the hypothesis that different life histories and habitat use can influence the number of distinct populations detected for these species along the Atlantic and Mediterranean considering only otolith shape. Further work will combine the use of multiple natural markers to better understand population connectivity and stock identification.

S4P7 Patterns and processes of genetic and species diversities in tropical reef fishes of the Western Indian Ocean.

Fabien Leprieur[1], Giulia, Donati[2], Maurine Vilcot[3], Stéphanie Manel[3], Camille Albouy[4,5], Loic Pellissier[4,5]

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Abstract

Generating genomic data for 19 tropical reef fish species of the Western Indian Ocean, we first investigate how species ecology influences genetic diversity patterns from local to regional scales. We distinguish between the α, β and γ components of genetic diversity, which we subsequently link to six ecological traits. We find that the α and γ components of genetic diversity are strongly correlated so that species with a high total regional genetic diversity display systematically high local diversity. The α and γ diversity components are negatively associated with species abundance recorded using underwater visual surveys and positively associated with body size. Pelagic larval duration is found to be negatively related to genetic β diversity supporting its role as a dispersal trait in marine fishes. Deviation from the neutral theory of molecular evolution motivates further effort to understand the processes shaping genetic diversity and ultimately the diversification of the exceptional diversity of tropical reef fishes. Then, we evaluate the similarity of diversity patterns across micro- to macroevolutionary scales using the same dataset. Our results reveal a strong correlation between genetic and species β-diversity, a result explained by the presence of a 'soft' barrier (i.e., the Monsoon drift) and mediated by larval dispersal processes. This suggests that vicariance and dispersal limitation are major processes shaping β-diversity patterns from microevolutionary to macroevolutionary scales in tropical reef fishes. We discuss the implications of these findings in the context of human impacts on tropical reefs.

S4P8 Human-mediated connectivity in the Atlantic as derived from maritime traffic arriving at Azorean marinas.

Authors: Ana C. Costa[1], Manuela I. Parente, Andrea Z. Botelho

[1]Faculdade de Ciências e Tecnologias and BIOPOLIS Program in Genomics, InBIO/CIBIO - Research Center in Biodiversity and Genetic Resources, Universidade dos Açores, R. Mãe de Deus 13A, 9500-321 Ponta Delgada, Portugal

Abstract

Humans have impacted marine ecosystems' connectivity through shipping activities for centuries. The introduction and dispersal of marine non-indigenous species are the iceberg tops of this change. By fouling or ballast water, these species can overcome distance and oceanographic barriers modifying benthic communities and shortening the distance of once isolated archipelago. In recent decades, the intensity of maritime traffic has grown, and so has the risk of NIS introductions. The Azores, an oceanic archipelago serving as a shipping hub for yachts crossing the Atlantic, has witnessed a growth in the number of non-indigenous species. Considering yacht fouling as one of the main drivers for artificially enhanced connectivity of marine Azorean communities, a preliminary risk assessment of introduction and establishment of NIS was made using as pressure proxies the official shipping data on the number of calls in port, last port call and the number of available berths and number of NIS reported in each marina of the archipelago. The most common international origin of marine traffic arriving in the Azores came from the Caribbean, and the island with the highest percentage of international traffic to arrivals to the island is the westernmost Flores. The marinas with an increased risk of NIS entry and, therefore, in which a monitoring effort should be intensified are besides Lajes das Flores, due to the reasons mentioned above; Horta (Faial island) due to the intensity of traffic it receives and Ponta Delgada on the size and number of registered NIS. High-risk marinas for the introduction of NIS should be monitored through regular NIS assessments and a detailed analysis of maritime traffic studying routes between the islands and among Atlantic archipelagos and both sides of the Atlantic to evaluate the magnitude of this human-mediated connectivity and identifying invading corridors.

S4P9 Habitat dependant growth of YOY Mugilidae at a limited geographical scale in South-Western Mediterranean.

Authors: Becheker Ali, Chaoui Lamya, Kara Mohamed Hichem

Marine Bioressources Laboratory, Annaba University Badji Mokhtar, Annaba, Algeria

Abstract

The five species of Mugilidae considered in this study (*Liza saliens, Liza aurata, Liza ramada, Chelon labrosus, Mugil cephalus*) breed at sea and fry recruitment takes place in different coastal habitats such as lagoons, estuaries or Posidonia meadows at Sea. The aim of this study is to compare daily growth of young-of-the-year (YOY) of these species according to coastal habitat type (lagoon, estuary, coastal sea) and to know whether habitat type influences the demographic structure of its occupants, which could impact connectivity measurement. Monthly fish sampling were carried out in four coastal habitats (Boukhmira and Mafragh estuaries, Mellah lagoon, La Caroube beach) with different abiotic characteristics and subject to different anthropic pressure. The daily age reading is taken on the lapilly otoliths of previously measured and weighed mugilidae individuals. The daily growth rate (mm/day) was calculated for each species at each site. *Liza saliens* fry (TL≤30 mm) is the most numerically present at Boukhmira estuary followed by Mellah lagoon and La Caroube beach. They are absent at Mafragh estuary and appears at this latter only from TL≥ 50mm. From TL≥ 110mm, they are present exclusively at Mafragh estuary and they leave the other sites. *Liza aurata* is present in all four sites with a numerical dominance at Boukhmira estuary. *Liza ramada* is present at Boukhmira and Mafragh estuaries, but less present at La Caroube and Mellah. *Chelon labrosus* is absent from Mafragh estuary and show a low numeric presence at the other sites. *Mugil cephalus* is present at Boukhmira estuary and El Mellah lagoon. The use of daily growth rates showed that *L. saliens* grows better during spring and summer in Mafragh estuary corresponding to the salinity increasing due to the opening of the estuary’s mouth. *Liza aurata* showed the highest growth rates from summer to winter in Boukhmira estuary which is constantly in contact with the sea and in Mafragh during spring. *Liza ramada* showed better growth in marine environments, while *C. labrosus* and *M. cephalus* showed better growth in lagoon environments during autumn and spring respectively. *Liza aurata*, *C. labrosus* and *M. cephalus* showed the worst growth rate at La Caroube beach which is subject to domestic pollution.

Theme session 5 - Using marine connectivity to inform management strategies and mitigate human impacts

24 May 2023

Conveners:
Ant Türkmen, LifeWatch ERIC, Italy
Burak Ali Çiçek, Eastern Mediterranean University, Cyprus

Marine ecosystems are connected – any management of marine habitats and species should be informed by marine connectivity to enhance recruitment, genetic exchange, and ontogenetic movement, as well as to avoid harmful connectivity of pathogens and pollutants. Marine resources are increasingly threatened, degraded or destroyed by human activities, reducing their ability to provide crucial ecosystem services. Important threats are, climate change, marine pollution, unsustainable extraction of marine resources and physical alterations and destruction of habitats and landscapes. Good governance, globally accepted targets, sustainable marine based human activities and adequate measures will be required to reduce the negative anthropogenic impacts on the marine environment. Projects and measures should ideally be designed and implemented in an integrated manner, in line with the ecological connectivity approach and involving all stakeholders.

This session aims to showcase examples of connectivity-smart management and challenges, and the approaches required to achieve this. Presentations will highlight how the ecological, biophysical, and social dimensions of connectivity can or have informed marine management.

S5 Keynote: Mediterranean Sea turtles: A model for understanding Marine Functional Connectivity.

Keynote: Robin Thomas Ernest Snape

SPOT - Society for the Protection of Turtles

Abstract

Some of the World's global leaders in natural science research have Mediterranean coastlines, so it's hardly surprising that Mediterranean Sea turtle populations are well-researched. After all, sea turtles are charismatic animals and so an excellent flagship for marine conservation. Sea turtles are also enigmatic, with complex life cycles which are challenging to unravel, and they thus naturally draw research interest and investment. This has driven the evolution of a toolbox of telemetry and molecular solutions to understand their connectivity. Through his talk, University of Exeter's Robin Snape will delve into the work carried out across the Mediterranean through the last half-century. Work that has led to an exemplary understanding of how this taxon of just a few species, use a global biodiversity hot spot, connecting the Middle East, Africa and Europe in collaboration.

S5O1 Design of new indicators using a larval particle transport model to assess connectivity processes in a northwestern Mediterranean Sea network of deep-sea no-take reserves.

Authors: Morane Clavel-Henry[1], Nixon Bahamon[1], Joan Navarro[1], Jacopo Aguzzi[1], Joan B. Company[1], Jordi Sole[2]

[1]ICM-CSIC
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Abstract

Providing ecosystem services such as seafood provisioning and protecting ecosystem health are key goals of marine ecosystem-based management. One management strategy is the implementation of Marine Protected Areas (MPAs), which contribute to habitats recovery and reestablishment of communities in highly impacted fishing grounds. A reliable recovery via the implementation of MPAs requires a thinking about the biological connectivity among a network of MPAs, modulated by time-dependent hydrodynamic and ecological factors. Spatial and time-variable connectivity indicators are required to picture the strength of adult and larvae flows across time but are presently missing in the literature. Here, we used a particle transport model coupled with an inter-annual hydrodynamic model of the NW Mediterranean Sea to obtain indicators of spatiotemporal connection along four recently established deep-sea no-take reserves (a type of MPA with full prohibition of fishing activity). Passive particles were released from the four reserves near the bottom and near the surface every month in three years that have strong differences in their hydrodynamic features (2008, 2014 and 2018) and tracked for one month. Then, a set of connectivity indicators will be created and related to the connection strength and occurrence among the four reserves and other more distant MPAs in the NW Mediterranean Sea. These indicators will be put into context of local hydrodynamics e.g. current velocities and mesoscale circulation patterns to better understand the physical processes affecting them. The present approach will allow the setting of adaptative management strategies in the incoming years to recover the populations of fishery-target or by catch species of different life strategies such as the decapod crustacean *Nephrops norvegicus*, the teleost fish *Conger conger*, the shark *Scyliorhinus canicula*, and the cephalopod *Eledone cirrhosa* along the whole network of MPAs in the NW Mediterranean Sea.

S5O2: Connectivity-based approach to guide conservation and restoration of seagrass *Posidonia oceanica* in the NW Mediterranean.

Authors: Ana Pastor Rollan[1], Andrés Ospina-Alvarez[2], Ignacio A. Catalán[2], Jorge Terrados[2]

[1] Aarhus University

[2] Mediterranean Institute for Advanced Studies (IMEDEA-CSIC/UIB)

Abstract

Posidonia oceanica is the most widespread seagrass species in the Mediterranean Sea. It is a key component of coastal seascapes across the Mediterranean marine ecosystem, where it plays fundamental ecological, physical, and economic roles. Although protection policies exist, *P. oceanica* meadows have been steadily declining in the recent past because of human activities and climate change. In the Balearic Islands, pressures are accentuated due to tourism and there is an urgent need to assess the connectivity of the *P. oceanica* patches as a key variable to guide the selection of source and destination areas to be protected and restored. In the present study a hydrodynamic model with high spatial and temporal resolution was coupled with hourly wind predictions to an individual-based model of *P.oceanica* fruits. We aimed to resolve the surface transport and dispersal of these fruits from semi-enclosed bays and near shore in an emblematic area in the NW Mediterranean. We use a graph theoretic approach to analyse the connectivity and, crossing this information with substrate suitable substrates, identify key seagrass protection and restoration areas. Connectivity analysis revealed high interannual variability in the dispersal probabilities, but some sites were highlighted as important for all years. This study shows how dispersal modelling and network analysis provide useful information that can be applied in conservation planning for key foundation species like *P. oceanica*, especially in regional integrated conservation management.

S5O3 Eelgrass genetic and biophysical connectivity assessments can identify critical sites for conservation.

Authors: Marlene Jahnke[1], Jonsson PR, Moksnes P-O, Loo L-O, Nilsson Jacobi M, Olsen JL, Serra Serra N, Kuusemäe K, Corell H.

[1]Department of Marine Sciences - Tjärnö Marine Laboratory, University of Gothenburg, Sweden

Abstract

The eelgrass *Zostera marina* is an important foundation species of coastal areas in the Northern Hemisphere, but is continuing to decline, despite management actions. The development of new management tools is therefore urgent in order to prioritize limited resources for protecting meadows most vulnerable to local extinctions and identifying most valuable present and historic meadows to protect and restore. In direct collaboration with, and partially funded by, Swedish management agencies, we assessed genetic and biophysical connectivity of eelgrass meadows along the Swedish coast. Both approaches were in very good agreement, and we therefore suggest that resulting genetic and oceanographic clusters should be used as management units (MUs). In fact, the suggested MUs correspond to a spatial scale appropriate for coastal management of "waterbodies" used in the European Water Framework Directive. The connectivity information can also be used to identify especially connected - valuable - meadows to protect, and lost meadows where restoration would best benefit the present metapopulation. Indeed, this data is starting to be implemented, and priority areas with high genetic diversity and high connectivity have been communicated to the County Administrative Board. Additionally, the European Commission has highlighted the importance and applicability of the approach by Jahnke *et al*. (2020) for assessing the efficiency of the EU's network of marine protected areas (MPAs) and defining management units (EU, 2020). In terms of eelgrass restoration, test planting has already been performed at several sites suggested as optimal restoration candidate sites. Finally, temporal genetic monitoring of eelgrass has now also been initiated in Sweden.

S5O4 Does connectivity between artificial reefs and MPA alter MPA network design? Case of study in the Gulf of lion (North West Mediterranean Sea).

Authors: Sylvain Blouet[1,2], Katell Guizien[1]

[1] CNRS-Sorbonne Université, Laboratoire d'Ecogéochimie des Environnements Benthiques, LECOB, Observatoire Océanologique de Banyuls Sur Mer, 66650 Banyuls sur Mer, France
[2] Ville d'Agde, Aire marine protégée de la côte agathoise, 34300 Agde, France.

Abstract

To halt the loss of biodiversity in accordance with the Convention on Biodiversity and the Aichi objectives, France aims to classify 10% of its territory as a strong protection zone by 2030. These new conservation zones will have to fit into the puzzle of marine spatial planning and respond in space and time to ecological, economic and social issues. In the Gulf of Lion, two complementary tools for the management of marine ecosystems, namely marine protected areas and artificial reefs, have been deployed. Artificial reefs were mainly submerged to support artisanal fishing and marine protected areas aim to conserve marine biodiversity. In this study, we aim at proposing prospective patterns of extension of conservation by the establishment of new marine protected areas. Scenarios were established using Marxan decision support software. Marxan uses a simulated annealing algorithm to implement the goal of achieving user-defined conservation targets such as amounts of habitat types or species as a representation of biodiversity and, where appropriate, connectivity constraints, while minimizing the overall cost of a system of marine protected areas. Two species of gorgonians with similar life history traits (*Eunicella singularis* and *Leptogorgia sarmentosa*) and whose colonization capacity in the study area is not limited by their pelagic lifespan or by currents were used as model species to test the creation of a network of marine protected areas in the Gulf of Lion. It was tested how the addition of population connectivity by larval dispersal between natural areas with and without the addition of artificial reefs influences the spatialization of the MPA network. These results constitute a first model for creating a network of conservation areas at a coherent scale that takes into account the connectivity between rocky habitats in the Gulf of Lion. They also provide answers on the effective integration or not of artificial reefs in the network of natural habitats.

S5O5 Population genomics of the Indian Ocean bigeye (*Thunnus obesus*) and skipjack (*Katsuwonus pelamis*) tunas provide management relevant information on stock connectivity.

Authors: Natalia Diaz-Arce[1]*, Iraide Artetxe-Arrate, Peter Grewe, Zulkarnaen Fahmi, Francis Marsac, Jessica Farley, Campbell R. Davies, Igaratza Fraile, Hilario Murua, Naiara Rodriguez-Ezpeleta

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Abstract

The efficiency of fisheries management plans, which aim at ensuring sustainability for commercial fisheries, can be severely compromised by an incorrect definition of management units or stocks. These management units are assumed to constitute naturally isolated populations whose parameters such as growth, recruitment and natural and fishing mortality are intrinsic and not dependent on emigration or immigration rates. Yet, mismatches between stocks and biological significant units are common in fisheries management, in part due to the difficulty to identify reproductively isolated populations, which is especially challenging in large migratory fishes such as tunas. Within the Indian Ocean, the bigeye (*Thunnus obesus*) and the skipjack (*Katsuwonus pelamis*) tuna are assessed each as a single stock even though studies based on fisheries catch data, parasite composition and tagging suggest potential sub structuring. Here, we have studied theirinter and intra-oceanic population structure and connectivity assembling for each species a dataset of about ten thousand genome-wide Single Nucleotide Polymorphisms (SNPs) from more than five hundred individuals of different age classes across the Indian and adjacent oceans. Our results support presence of structural genomic variants distributed at different frequencies across the Indian Ocean, suggesting the presence of partially isolated groups, and which for both species also suggest genomic permeability between oceans: Atlantic and Indian in the skipjack tuna and Pacific and Indian in bigeye tuna. The observed connectivity patterns challenge the current single stock-based assessment while demanding additional analyses to better understand the role of these genomic structural variants on the adaptive potential of these species to a changing environment. Altogether, these results highlight the benefits of genomics-informed management and conservation strategies in tropical tunas.

S5O6 Connectivity matrices for a sustainable management of mussel aquaculture.

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Abstract

Spain is the second mussel producer in the world with an average annual production of 250.000 tonnes which comes mostly from the NW region (Galicia). Mussel aquaculture in Galicia is performed on embayments called “Rías” and sustained on mussel seed collection from rocky shores, which means an annual harvest of 7.500-9.000 tonnes of seed scrapped directly from the intertidal. During the last couple of years the availability of mussel seed is decaying, so a proper spatial management of this resource, identifying the main “source” and “sink” sub-populations is increasingly being demanded. The geochemical composition of calcified structures of marine organisms reflects geographical differences in water chemistry. Therefore, bivalve shell geochemistry is increasingly being employed as a natural tag to discriminate among source populations and understand connectivity patterns and larval dispersal patterns. Here we developed a series of “in situ” larval cultures of mussels at two neighbourgh embayments were the mussel aquaculture is performed (Ría de Vigo and Ría de Pontevedra), which allowed us to identify site-specific signals for each Ría with a high reclassification success (96% of jackknifed cross-validated cases correctly classified) based on 3 of 13 trace-elements analysed (Co, Ba, Ce). The analysis of the larval shells of recruits collected at each embayment, allowed us also to assign them to a natal origin and calculate connectivity matrices between both Rías. Self-recruitment was the most important source of juveniles for both Rías (43-53%), but interchange between both neighbourgh Rías was significant (21-31%) and complemented with a relevant percentage (26%) of larvae coming from other unknown sources. These results validate the elemental fingerprinting technique to study the fluxes of individuals between the Galician Rías, and it’s the first step towards the implementation of an integral spatiotemporal management strategy.

S5O7 Ecological connectivity in marine protected areas in Swedish Baltic coastal waters - a coherence assessment.

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Abstract

Networks of marine protected areas (MPAs) are increasingly being established to safeguard and restore species and habitats threatened by human activities. We assessed the ecological coherence of the MPA network along the Swedish Baltic Sea coast, focusing on ecological connectivity and representativity, and species performing active migrations which dominate in the ecosystem. We also tested the influence of anthropogenic pressures on connectivity and identified areas for expansion of the existing MPA network to maximise connectivity in the region. Maps of species distributions produced by statistical modelling were combined with information on dispersal distances to produce connectivity maps, using a degree centrality approach. Hotspot areas for connectivity were identified, and these were generally concentrated in a few, relatively small, areas along the coast. These hotspot areas are, however, highly susceptible to coastal development and human activities, as they are often situated in bays, inlets and archipelagos where human development coincides with sensitive vegetated habitats and important spawning, nursery and feeding grounds for fish. Physical disturbance from boating, construction, dredging etc., was estimated to have a relatively large impact on connectivity, particularly on species of freshwater origin and with short migration distances (e.g. cyprinid species). This includes large predatory fish like pike, pikeperch and perch, as well as habitat-forming vegetation, which showed a pronounced decrease in connectivity when incorporating physical disturbance into the models. Representativity, i.e. the amount of habitats protected, was generally below the new target of 30% protection by 2030 in the EU Biodiversity Strategy. Similar results were found for connectivity where the amount connected habitat within MPAs was low. Priority areas for connectivity, identified by the spatial prioritization software prioritizr, were insufficiently protected, and the connectivity of the network could be greatly improved with targeted protection in just a few important locations.

S5O8 Measuring interconnectedness between marine ecosystems and socio-economic activities: an accounting approach.

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Abstract

Marine ecosystems and their services are under unprecedented threats. Climate change, invasive species, pollution and overfishing mine the integrity and health of the ocean, and developing a holistic approach has to be a of Europe's response to global challenges. For this reason, planning and managing sustainable development of socio-economic sectors and marine resources requires an all-encompassing knowledge of marine environment, which also includes the marine functional connectivity. Here we will present how marine connectivity could be directly included in the framework of European legislations, ranging from marine biodiversity monitoring, ecosystem condition to the accounting of marine ecosystem services and to economic sectors, households and global society. There is in fact a cause-and effect relationship that can quantitatively link changes in marine ecosystems to economic and social impacts. Finally, we will discuss the potentialities and challenges on including marine connectivity data for mapping and assessing ecosystem condition in terms of the implementation effectiveness and sustainability of conservation, protection and restoration actions for achieving clean and healthy oceans.

S5O9 Spatial Conservation Priorities with Connectivity in The Eastern Mediterranean.

Authors: Burak Ali Çiçek[1], Ant Türkmen, Mustafa Soğancı, Ilaria Perriu, Robin T. E. Snape, Damla Beton, Pierre Marchat, Buki Rinkevich, Andreu Blanco, Manuel Hidalgo Roldan, Andres Ospina-Alvarez, Thanos Dailianis, Marco Andrello, Anna M. Addamo, Nazlı Demirel, Aylin Ulman, Servet Doğdu, Umar Khan, Tamar Guy-Haim, Andreas Reul, Gil Rilov, Zacharoula Kyriazi, Yael Teff Seker, Aytaç Özgül, Adla Kahric, Alan Rees, Gail Schofield, Yaniv Levy, Shir Sassoon, Aliki Panagopoulou, Onur Candan, Eyüp Başkale, Oğuz Türkozan, Ali Fuat Canbolat, Annette Broderick, Brendan Godley, Maria Bege

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Abstract

Marine functional connectivity (MFC) is important for designing spatial management areas and improving management plans. Today, the threads facing marine ecosystems include the impacts of invasive or non-indigenous species, overexploitation, pollution and climate change. Especially, climate change and rapid spread of invasive species are two significant threats to marine biodiversity worldwide. Therefore, knowledge on MFC becomes even more relevant in the light of the current effort towards restoration of marine habitats, being essential for maximisation of the benefits and the soundness of the proposed actions that sustain a diversity of ecosystem services. Contrastingly, the same processes we hope to support to maintain biodiversity and ecosystem functions also underscore the spread of invasive species. The Eastern Mediterranean Sea forms a testbed case for examining contrasting conservation objectives for spatial planning in regard to connectivity. Here we use animal movement tracking, biophysical modelling, genetic data and observations of invasive species spread to determine conservation priority areas. We compare priority areas and conservation benefits for a range of conservation objectives, as follows: a) maximise connectivity for native species; b) disrupt the spread of invasive species; c) combining the needs of native and invasive species management, and the counterfactual, d) planning without connectivity. Results revealed that there are substantial trade-offs in contrasting objectives to support versus disrupt connectivity when only one management action (protected areas) is considered. However, there can be remarkable spatial synergies when considering different management actions, such as protection and strategic control of invasives. Nevertheless, many invasive species are here to stay, and conservation planning objectives that support native species protection are key to ensure their adequate management.

S5O10 The South Adriatic Ionian Straight Ecologically or Biologically Significant Area (SAIS-EBSA), informing regional seas and high seas governance.

Authors: Peter Charles Mackelworth[1], Caterina Fortuna[2], David Rodriguez Rodriguez[3], Dania Abdul Malak[3], Draško Holcer[4]

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Abstract

More than 300 Ecologically or Biologically Significant Areas (EBSAs) have been archived by the Convention on Biological Diversity (CBD) worldwide. These are special areas that support the healthy functioning of oceans and its ecosystem services, often identified for the presence of wide ranging or migratory species of conservation concern. Although the listing of an EBSA has no direct implication for management, the CBD COP 10 emphasized that the selection of conservation and management measures in an EBSA is a matter for States and competent intergovernmental organisations, in accordance with international law. Considering that many of the EBSAs are large transboundary areas incorporating different national jurisdictions as well as the area beyond national jurisdiction (ABNJ), maintaining their functional connectivity through appropriate governance mechanisms may be complex. As part of the Mediterranean Interreg programme, the Mediterranean Biodiversity Protection Community aims to facilitate the development of appropriate governance in the pilot site of the South Adriatic Ionian Straight (SAIS) EBSA. The SAIS-EBSA site provides insight into the roles of the regional intergovernmental organisations and their interactions with the contracting States, particularly the EU macro regional strategy for the Adriatic-Ionian Region and the UNEP/MAPSPA/RAC. It is clear that engagement with the Blue Growth agenda and integrating maritime spatial planning and marine conservation agenda is essential. The systematic identification of spatially defined conservation areas within the SAIS-EBSA can contribute to the 30% of effective area-based conservation measures by 2030, identified by the CDB and EU. Effective governance in the SAIS-EBSA has the potential to inform governance in other EBSAs and hence contribute to global conservation goals. Finally, it is anticipated that the EBSAs will play an important role in the discussions surrounding the development of a new international legally binding instrument (ILBI) for the conservation and sustainable use of marine biodiversity in the ABNJ.

S5O11 Designation of and Connectivity in a Habitat Directive Marine Protected Area: The Case of the Transboundary North Sea Dogger Bank.

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Abstract

In the past designation of Marine Protected Areas (MPAs) under the EU Habitats Directive followed a procedure that was strongly Member State driven. For shared features this led to differences in objectives, data used, and timing. This will be illustrated with the Dogger Bank: a submerged sandbank in the middle of the North Sea that is shared by four countries (UK, NL, D and DK). In 2011, the intergovernmental Dogger Bank Steering Group started a transboundary process for the Dogger Bank, in order to enable designing a coherent transboundary fisheries management plan to achieve shared conservation objectives. Due to the Member State driven nature of the Habitats Directive many obstacles needed to be cleared. Ultimately, common ground was found, and a fisheries management spatial proposal was agreed on for the transboundary area. This proposal includes specific national objectives, and also notions for ensuring local connectivity. Due to the complexity of the transboundary process and adopting fisheries measures under the EU Common Fisheries Policy (CFP), it took until 2019 for a management proposal to be submitted to the EU, and as a result of Brexit an amended plan, excluding the UK, was submitted in 2021. I will argue that the bottom-up process that was followed had very little consideration for connectivity issues, and will illustrate this with a Sand Eel example.

S5O12 Integrating spatial ecology into marine spatial planning.

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Abstract

Marine Spatial Planning (MSP) aims to reconcile maritime uses with the marine environment. Rapid use-oriented development throughout the coastal ocean often neglects marine environmental integrity under MSP. However, the marine environment creates and sustains numerous maritime uses, which calls for an improved recognition of its components and processes in MSP. This situation leads to difficulties in modeling and describing the marine environment because complex ecological processes and conflictual uses of resources often coexist and are interconnected. Providing MSP with spatially explicit information on hotspots of biodiversity and biomass can improve ecosystem based management under best available science. Altogether, this approach supports MSP with ecologically relevant patterns of spatial distribution and connectivity for decision-makers. We present a case study focusing on the maritime spatial plan of the German EEZ in the Baltic Sea, illustrating hotspots of demersal fishes. Maps will be produced, which can be put in direct relation with maritime uses, emphasizing borders and boundaries of MSP from an ecological perspective. For example, they shall include expected energy projects, species distribution hotspots and how this information can be made spatially relevant to inform MSP. This approach aims to broaden nature protection management by highlighting the importance of multi-species targets, which are heterogeneous in space. Our work demonstrates that existing ecological data can be used to enable holistic MSP.

S5O13: MarinePlan: Ecosystem based maritime spatial planning in the Celtic Sea.

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Abstract

One of today's most pressing challenges is to conserve and restore biodiversity and functioning, while simultaneously allowing for their exploitation by those who depend on their services, goods and benefits. In Europe, Maritime Spatial Planning (MSP) is the main governance process to ideally connect sustainability and exploitation. MarinePlan is a European project which will co-develop with stakeholders a Decision Support System (DSS) for ecosystem-based maritime spatial planning (EBMSP). The DSS will be developed and applied at eight European planning sites, one of which is the Celtic Sea. The Celtic Sea is a key fishing grounds as well as an area of high biodiversity but has also been identified as an important area for offshore windfarm development. By 2030 Ireland must protect 30% of its marine area as well as meeting a target of generating 7GW of energy from offshore renewables. In order to meet both of these targets, while retaining the viability of the fishing sector it is imperative to incorporate the planning of any new marine artificial structures with existing socio-economic activities and the designation of Marine Protected Areas (MPAs) and to develop and apply criteria for MPA connectivity. MarinePlan will apply an integrated approach in the Celtic Sea to enhance the design and effectiveness of spatial conservation and restoration measures. It will identify areas for conservation by using criteria for ecologically or biologically significant marine areas (EBSA) whilst also engaging with stakeholders in the planning sites to understand societal needs and concerns in relation to maritime spatial planning. We present the approach the Celtic Sea Case Study plans to use to connect ecological, biophysical and social dimensions, how it hopes to inform marine management and the challenges we expect to face.

S5P1 Ecological-economic modeling of nutrient enrichment in multi-species fisheries.

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Abstract

In fisheries economics, multispecies or ecosystem models often focus on interactions of fish species, especially the interdependence between species in a prey–predator system. An ecosystem approach means different things to different people. As a result the concept of ecosystem-based fishery management is evolving and it has no universal definition or consistent application. This paper investigates the dynamic of an ecosystem by adding the effects of nutrient enrichment on a predator-prey system. Nutrients mentioned in our model are understood as elements that are essential to the structures and functions of organisms such as nitrogen, phosphorus, potassium and calcium. Given the assumption that harvest of the predator stock is a linear function of the control, and harvest of the prey stock is not economical, we investigate stability of the ecosystem under the influence of nutrient enrichment and fishing. We also establish the existence of a steady-state interior equilibrium and describe the approach path to it.

S5P2 Assessing the potential for mesophotic coral reefs to ensure the survival of shallow coral reefs.

Authors: Colin Scherpereel[1], Daniel M. Holstein[2], Thomas Dobbelaere[1], Jonathan Lambrechts[3], Emmanuel Hanert[1,3]

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[3]IMMC, UCLouvain

Abstract

Mesophotic coral ecosystems (MCEs), located at depths greater than 30m, are one of the last lifeboats for coral reefs worldwide. Being partly sheltered from global warming, they could fare better than shallower coral reefs in the next decades and help repopulate them through larval exchanges. The United States Virgin Islands (USVI) are home to some of World's richest and best documented MCEs. However, these islands are highly threatened by the spread of the stony coral tissue loss disease (SCTLD). The transmission of the SCTLD is likely to be supported by the dispersal of fine sediments transported by the same ocean currents responsible for larval exchanges. As connectivity can be a double-edged sword, it is therefore particularly challenging to identify which reefs are best suited to protection/restoration efforts. Here, we aim to assess the contribution of USVI MCEs to the resilience of the entire coral ecosystem. More specifically, we simulate the dispersal of larvae and disease agents thanks to a Lagrangian transport model coupled with a three-dimensional unstructured-mesh hydrodynamic model to deal with the USVI's deep and steep bathymetry. We then identify the best larvae exporters and weakest disease importers in the connectivity networks by deriving conservation metrics based on graph theory algorithms. We consider different species with various susceptibilities to SCTLD and various larval traits in order to account for the USVI's coral diversity. This allows us to highlight the MCEs with the most positive impact on the entire coral ecosystem and that should therefore be protected/restored in priority. In addition, we give a quantitative estimate of MCEs' contribution to shallow larval recruitment and inform on the potential of the SCTLD to reach mesophotic reefs and spread among them.

S5P3 Genetic connectivity assessment to inform marine protected areas establishment: a case study of an isolated fish population in the Southwestern Atlantic.

Authors: Julia Tovar Verba[1], Linda Hagberg, Maria Grazia Pennino, Carlos E. L. Ferreira, Priscila F. M. Lopes, Beatrice Padovani Ferreira, Sergio Maia Queiroz Lima, Adam Stow

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Abstract

Despite the lack of obvious barriers, populations of marine organisms can present different levels of connectivity throughout their distribution. The degree of connectivity between populations of exploited species should be considered when defining conservation measures. Here we investigated the genetic connectivity of the endemic and exploited Gray Parrotfish, *Sparisoma axillare* in Brazil. This vulnerable species is exploited and there is a dearth of ecological data needed to support sustainable management actions and protected areas implementation. Nine locations were sampled from reef systems in coastal to oceanic environments with varying levels of protection. The combination of depth, ocean currents, and distance were the major drivers explaining patterns of genetic divergence between *S. axillare* populations. Samples from six coastal sites and from two off-coast sites showed high levels of connectivity. An isolated and genetically distinct population was revealed in the waters surrounding Trindade island, located 1000km off-coast. Despite the Seamounts of Vitoria-Trindade Chain work as a connection between coast and Trindade island for several fish species, including some from the same genus, it does not seem to be for *S. axillare*. This indicates that, even species with shared life and evolutionary histories, levels of genetic connectivity can strongly vary. Our results have important management implications: a large no-take area has recently been established in part of Trindade island, increasing country's marine protection. However, this loosely regulated area is located in the open ocean, leaving out shallow areas. Despite bans to fisheries, these areas are still exploited. Granting Trindade full protection would provide a response to criticisms and give some respite to a unique and isolated *S. axillare* lineage.

S5P4 Connecting people co-creating management tools through participative process to safeguard marine natural resources in complex socioecosystems.

Authors: Alfredo García de Vinuesa[1], David Florido[2], Cesar Vilas[3], Marcos Llope[1]

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Abstract

Most of the Gulf of Cadiz commercial species stocks, such as anchovy or shrimp, depend to a great extent of their connection with the nursery area located at the Guadalquivir estuary and neighbouring waters. Hence, the environmental conditions at this essential fish habitat ultimately have an effect on the Gulf of Cadiz fisheries. The Guadalquivir estuary supports a great number of anthropogenic activities such as agriculture, aquaculture, illegal fishing, mining or shipping. Consequently, these human sectors exert cumulative impacts over it nursery role. The social system around the Estuary is especially complex and its network arrangement is characterised by homophilia patterns (i.e. preference for intrasectoral interactions). These social features result in a relatively low intersectoral connection, needed for marine resources management. Participative processes have proven useful to establishing intersectoral connections and engaging stakeholders in the management, improving marine resources conservation. In addition, conceptual modelling is an intuitive tool, easy to use with stakeholders, suitable to extract local/fishers ecological knowledge and to eventually co-create accepted and legitimated frameworks. In this context, we are carrying out a participative process and, by means of mental modelling, co-creating the first conceptual map that couples the ecological and social facets of the Guadalquivir estuary-Gulf of Cadiz system. This model will serve to assess sectoral trade-offs and propose management strategies that result in a virtuous balance within the ecosystem boundaries, including anticipated future challenges like climate change effects.

S5P5 What lies beneath. Biodiversity and structure of infaunal understory assemblages structured by the habitat- forming seaweed *Ascophyllum nodosum* (L.) and their response to cutter rake harvesting.

Authors: Neve McCann[1], Jose M. Farinas

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Abstract

Bladderwrack *Ascophyllum nodosum* is a common intertidal seaweed that is mostly found in rocky sheltered locations. This is a habitat-forming, keystone species that is also of major importance to the local economy. It is commonly harvested along the west coast of Ireland for an assortment of uses. Common inhabitants of *A. nodosum* canopy include a multitude of benthic invertebrates that rely on the seaweed for shelter and protection. Thus, assessing the impacts of harvest on the under-canopy residents is crucial to sustainably managing this resource as it supports the instilment of biodiversity. The current study aimed to characterise the community structure and determine the influence of *A. nodosum* harvesting on the biodiversity of associated benthic invertebrates at two different harvesting sites along the west coast of Ireland in Galway Bay (Roundstone & Kinvara). Three sampling visits using a BACI approach (i.e., before harvest baseline, and two surveys after the harvest) were carried out at each site over the course of a year. Additionally, sampling was carried out at one of the sites due to unexpected overharvesting. Sorting and taxonomic identification took place prior to statistical analyses, which determined differences in invertebrate biodiversity at each site over the course of the surveys. Results indicated a significant temporal difference in community structure at each site after harvesting. The community structure in Roundstone was generally much more homogeneous and less variable than Kinvara. Additionally, the results suggest an overall loss in species composition initially after harvesting; while some long-term recovery was observed in plots where harvesting was regulated to 30% biomass extraction. This was not the case in the overharvested plot which showed no extensive recovery in biodiversity after one year, highlighting the importance of sustainable harvesting for a healthy ecosystem.

S5P6 Who are the potential marine benthic colonizers of offshore wind farms within the English Channel using diversity and functional traits analyses?

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Abstract

In the next decade Offshore Wind Farms (OWF) are planned to be implemented in the English Channel and these artificial structures will impact the marine ecosystems structure and functioning through, for example, the reef effect. The North Sea and the English Channel already hosts artificial structures like oil and gas platforms (O&GP) that generate a reef effect as well as hard substrates (HS) that are colonized by benthic organisms. The question to be addressed in this study is to compare the diversity and functional traits of the benthic communities of OWF, O&GP and HS in order to identify a functional profile of the colonizers of future OWF. Based on an extensive literature review, a community analysis (PERMANOVA and then Hierarchical Ascending Classification) has been performed. Results revealed a greater similarity between the communities of OWF and O&GP compared to the communities of HS. A second approach, using functional traits analysis, has been applied on the commonest species. Functional traits analysis has shown that during their intermediate stage of development, benthic communities of OWF, have a similar functional richness and diversity (0.68 and 0.53 respectively) than the communities on the HS (0.54 and 0.5 respectively). But using O&GP as a long-term view of the colonization for OWF, functional richness and diversity may decrease during the climax stage (0.07 and 0.42 respectively). In both habitats, pelagic and planktotrophic larvae were the most represented categories. Such traits could help species to disperse in the environment. These results will be used to identify the future colonizers of OWF whose larval dispersal could be studied in order to explore the stepping stone effect that could be generated as a consequence of the increase of OWF within the English Channel.

S5P7 Demystifying marine functional connectivity in spatial conservation prioritisation.

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Abstract

Connectivity is among the most important ecological processes that support the persistence of life on earth, and therefore it needs to be a key criterion in conservation decisions. Many managers and conservation experts understand the importance of connectivity, the flow of organisms, materials and energy across space, but it remains difficult to use connectivity information in spatial planning. Connectivity is nebulous, it can be abstract and mean different things to different people, making it difficult to include in conservation problems. An important challenge is to translate the flows associated with connectivity into conservation objectives that lead to management or conservation interventions. Accepted best practice for spatial conservation planning defines objectives and the environment to protect in quantitative (mathematical) terms. This process identifies sets of candidate conservation and management areas that together achieve the conservation goals, whilst minimising the cost to and conflict with resource users. Greater computing power, new models, and technology have facilitated a much-improved quantification of connectivity, but also introduced new challenges. Diverse ways of living, growing, and reproducing mean that species have very different connectivity and thus conservation needs – what a lizard needs is very different from an elephant. I will point to the importance of conservation decisions overcoming the narrow range of life histories typically used to represent the possible connectivity space in a land- or seascape, and summarise a broad overview of tackling the bottleneck of delivering connectivity as a global policy ambition in spatial conservation: a disconnect between connectivity science and practise that we will need to tackle with co-learning and interdisciplinary planning.

S5P8 Assessing Long Distance Dispersal patterns and connectivity of *Macrocystis pyrifera* in the Chilean coast.

Authors: Gabriela Thompson-Saud[1], Alana Grech[1], Sebastian Vasquez[2], Andres Ospina-Alvarez[3]

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Abstract

Dispersal and connectivity play crucial roles for kelp forests, including replenishment and recovery following disturbance events, maintenance of population structure at the scale of the distributional range of species, supporting genetic diversity and responding to invasive species and transmission of disease. The dispersal capacity of *Macrocystis pyrifera* suggests the existence of metapopulations, where discrete habitat patches or groups of patches form subpopulations that interact at some level. Here, we analysed dispersal and connectivity of *M. pyrifera* communities in the Chilean coast. This work aimed to improve understanding of metapopulation dynamics, population structure and to inform the giant kelp management and conservation. For this purpose, a hydrodynamic model of the Southeast Pacific region was coupled with an Individual Based Model that captures the biological parameters of the kelp. The outputs were analysed to infer areas with high connectivity. Centrality measures, such as in and out-strength, closeness and Eigenvector were used to find the most important areas for the giant kelp along the coast. Additionally, spatially-explicit scenario analyses were conducted to understand connectivity structure changes under future disturbance regimes. We identified key areas of connectivity in the southern part of Chile and a tendency of connectivity from south to north. We also observed that the dispersal occurs over international boundaries and assessed the implication for the giant kelp management. This study provides important insight into the use of biophysical models to understand a crucial aspect of the giant kelp population connectivity and key information to inform future management plans.

S5P9 Building a model-based coral connectivity atlas of Florida’s Coral Reef.

Authors: Thomas Dobbelaere[1], Joana Figueiredo[2], Daniel D Holstein[3], Emmanuel Hanert[4]

[1]Earth and LIfe Institute, UCLouvain
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Abstract

Coral populations have experienced a world-wide decline due to both global and local anthropogenic stressors and almost all live coral cover could be lost under a >1.5°C warming. Avoiding climate change being no longer an option, local actions are required to mitigate its effects and support coral recovery. To maximize the resilience of large-scale reef systems with localized actions, knowledge about the connectivity between reefs is needed. These exchange processes are driven by currents with complex small-scale circulation features within reef systems. Hence, biophysical models that can simulate the life-traits and transport of coral larvae down to the reef scale are required to estimate coral connectivity. However, due to the important computational cost of such models, connectivity studies often consider a small number of coral species over a limited number of spawning events, therefore lacking interannual and inter-specific variability. Here, we used the multi-scale ocean model SLIM to simulate the dispersal of larvae from 7 coral species in Florida’s Coral Reef over 10 consecutive years (2012-2022). We then computed connectivity metrics to identify the reefs best suited for protection and restoration efforts over multiple years and multiple species. By identifying similar spatial patterns in connectivity measures between species, we highlight the potential for coupled restoration. Furthermore, using 10 years of modeled larval dispersal, we build robust estimates of long-term connectivity. Such estimates could be used to predict the potential evolution of the reef system and bridge the gap between genetic connectivity and larval dispersal in Florida’s Coral Reef. This study provides unprecedented easy-to-access reefscale connectivity datasets to inform the design of future marine conservation strategies.

S5P10 Coupling natural and electronic tags to explore spawning site fidelity and natal homing in northeast Atlantic European seabass.

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Abstract

Ecological evidence is missing to support the current stocks delineation of European seabass. Adult spawning site fidelity and natal homing were analysed by coupling Data Storage Tag (DST) information and otolith microchemistry of recaptured fish to investigate, within the study area, the population structure and connectivity in European seabass. Trajectory reconstructions inferred from DST data were used to assign a spawning area (English Channel or Bay of Biscay) to each spawning winter record. In addition, otolith composition (Mg, P, Mn, Zn, Sr, Ba and δ18O) was measured in both larvae and adults otolith increments corresponding to a winter spawning event. We built a training dataset using coupled spawning area assignments and otolith elemental signatures for winters with DST data. The training dataset was used to calibrate a Random Forest model and assign spawning areas based on otolith winter signatures outside the DST recording period. Results revealed that 64 % of the seabass expressed spawning site fidelity. We also found a geographical gradient of site fidelity, with the highest proportions of spawning site fidelity found in seabass tagged at the northern and southern limits of the studied area. Significant ontogenetic effects were observed for trace elements and δ18O with ratios significantly lower in the larval stage than in the adult stage. These biases and the variability across cohorts prevented us to use the assignment model fitted on adults to study natal homing. At the larval stage, the analysis of spatio-temporal effects on otolith trace elements did not reveal any significant difference between spawning areas. However, the patterns of difference were similar for larval and adult Zn, Sr and Ba between the two spawning areas, suggesting a homing behaviour.

S5P11 Connectivity and divergence of deep-sea mussel *Bathymodiolus septemdierum* complex across the Indo-Pacific vent region.

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Abstract

Deep-sea minerals such as polymetallic nodules, hydrothermal vent sulphides, and seamount-associated crusts are considered as possible alternatives to terrestrial metal resources. Deep-sea mining activities without environmental impact assessment would significantly cause a negative impact on these minerals associated deep-sea ecosystems and raise concerns about harming the habitat integrity, biodiversity, and their ecosystem services. Integrating genomic and oceanographic approaches could be insightful in providing knowledge on the distributions and connectivity of associated species to establish a management plan to protect these deep-sea habitats. Deep-sea mussels (Bivalvia: Mytilidae) are ecologically important species in the deep sea, particularly, *Bathymodiolus septemdierum* complex is widely distributed in the Indo-Pacific hydrothermal vents. Yet, how their dispersive larvae establish connections between remote populations remains unclear. Here, we analysed 114 individuals from eight vents in the Indo-Pacific region incorporating 96,213 single-nucleotide polymorphisms by whole genome re-sequencing for population genomic analyses and high-resolution ocean modelling. The population genetics analysis confirmed the population subdivision between the Indian Ocean and the Pacific Ocean and further diversification between the north and the south Indian Ocean. The contemporary connectivity of the *B. septemdierum* complex revealed that Lau Bain might be the stepping-stones habitat to connect the Indo-Pacific vent sites and help Bathymodiolin mussels disperse widely. Our study provides strong evidence to decipher how the vent systems are biologically connected between widely separated vent habitats and provide suggestions on conserving deep-sea biodiversity and establishing marine protected areas.

S5P12 Relational ties with fishers and consumers contribute to fishers' conservation mindset.

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Abstract

Despite the increasing need for fishers and seafood beneficiaries to cooperate in natural resource governance, little attention has been paid to the relational value between fishers and consumers for fisher's conservation mindset and behavior. The case of Onna village is a unique example that fishers actively engage in nature conservation activities not only sea-based activity (i.e., coral cultivation and planting) but also in-land activity (i.e., prevention of red clay outflow). Onna Village has a beautiful 27 km coastline consisting of coral reefs and white sandy beaches, and this long coastline is designated as Okinawa Coast National Park. This study demonstrates the influence of the opportunity to interact with "outsiders" on fishers' nature conservation mindset through quantitative and qualitative data obtained in Onna village, Okinawa, Japan. The Onna village fishery cooperative has been collaborating with the Onna Village Corp Coral Forest Liaison Group and organizing social gathering events for fishers and consumers to interact with each other since 2009. The consumer side participants of those events are from outside of Onna village, all of them are contracted coop members, and visit there to learn about the Mozuku (seaweed) production processing and local culture. The qualitative and quantitative research shows that fishers in Onna village have a high tolerance for outsiders, a high level of normative awareness, and high internality. Internality has a collation with life satisfaction and tends to take proactive action to solve problems, with a disposition to attribute results to internal factors such as one's efforts. The fishers' primary job is cultivating seaweed in Onna village, and interacting with consumers and conservation activities needs additional efforts and costs. Nevertheless, this research suggests the value of investing human capital and non-directly fishing activities at fishery cooperatives for future sustainable fisheries and long-term development in coastal areas.

S5P13 Genomic characterization and population connectivity of wild and farmed blue mussels (*Mytilus* spp.) in Irish waters.

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Abstract

The edible blue mussel (*Mytilus* spp.) is an ecologically and economically important bivalve commonly found in the wild around the Irish coast. It comprises two congeneric species, the Atlantic Mytilus edulis, and the Mediterranean *Mytilus galloprovincialis*, and their fertile hybrids. A substantial knowledge gap exists on the taxonomic status, genomic composition, population structure, and connectivity of Irish mussels, as well as the dynamics between farmed and wild stocks. To address such gaps, genetic analyses were conducted on wild and farmed mussels' stocks from 30 locations around the Irish coast. Preliminary analysis using a single marker approach (adhesive protein) showed a prevalence of M. edulis followed by hybrids and a minor presence of *M. galloprovincialis*, mainly on the south and west coast. However, this methodology has limitations and does not provide an in depth insight on levels of hybridization and introgression (e.g. beyond F1 hybrid generation). Thus, a multi-marker genetic analysis employing Single Nucleotide Polymorphisms (SNPs) has been conducted in order to refine the taxonomic composition of the studied stocks. A panel of 91 SNPs was selected from previously published studies, with the aim of conducting genotyping using a high-throughput qPCR platform (Biomark HD, Standard BioTools). Following protocol optimization, a pre-amplification step is recommended for samples with low starting genomic DNA. Genotyping up to 1,000 individuals is ongoing and findings will be presented to show taxonomic composition around the Irish national coastal territory. Results from this study will allow the characterization of Irish mussel stocks, providing insights on sustainable shellfish farming practices as well as levels of connectivity among wild mussel populations.

S5P14 Contribution to the knowledge of population structure and connectivity of two coastal pelagic fish through a multi-method approach.

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Abstract

Efficient management of fisheries implies that the stock structure and connectivity of the target species are well understood to allow the design of appropriate management regulations in fisheries. Without an understanding of population structure and species connectivity, fisheries can put unexpectedly high pressure on specific regional populations, resulting in the overfishing of some stock components. In Portugal, Atlantic chub mackerel (*Scomber colias*) and European sardine (*Sardina pilchardus*) are economically important and the most captured species. Currently, for *Scomber colias*, there is no stock management for Atlantic European waters, and its population structure remains unknown. For *Sardina pilchardus*, stock delineation for management purposes remains unclear and is often under debate. For that, the objective of this study is to contribute to the knowledge of *Scomber colias* and *Sardina pilchardus* stock structure in Atlantic and Mediterranean waters and to understand if there is a spatial genetic structure (genetically distinct populations), a morphometric structure at a geographic level (phenotypically distinct populations) and the degree of reproductive isolation of these populations (connectivity). Final and preliminary results of the population structure (and its connectivity) for *S. pilchardus* and *S. colias*, respectively, as well as the consistency/correspondence among applied techniques, will be presented. Individual migration among adjacent areas and even beyond well-defined geographical barriers such as the Gibraltar Strait, among Atlantic and western Mediterranean locations, were pointed. The results of this work improve the understanding of the species' population dynamics and can enlighten models from a biological perspective, helpful to management strategies information, and consequent human impacts mitigation on these species.

S5P15 Local ecological knowledge networks in tropical artisanal shrimp fisheries.

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Abstract

Local ecological knowledge (LEK) in fishing communities is generated through interactions between fishers and the exploited resources. It is transmitted through social networks, tools that are useful for analyzing the socio-ecological systems' dynamics (SES). LEK variability is supposed to depend on the quality and quantity of ecological information flow among different stakeholders. To assess what is driving LEK themes, we hypothesized that the formation of LEK clusters among fishers is determined by network articulation, fisher experience, and the exploited species' commercial value. The study area comprises three fishing communities in the Western South Atlantic, in Brazil's tropical coastal zone, where artisanal shrimp fisheries (on *Penaeus schmitti*, *P. subtilis* and *Xiphopenaeus kroyeri*) are a major activity. Data collection took place between March, April, and November 2019. To test our hypothesis, linear regression and bipartite network analyses were performed to visualize the interactions between fishers groups and LEK themes. This social network's connectivity, nesting, modularity, and centrality parameters were calculated to test the hypothesis. Our results indicate that experienced fishers perceive their LEK as large enough to be revealed in their networks on food, mortality, and growth themes. Furthermore, there are subgroups of fishers with dissimilar knowledge about the exploited shrimp species, one old on the fishery with broad knowledge, other less experienced, just knowing about reproduction and migration themes. We conclude that there is a spatial similarity in the connectivity of fisher's LEK, mainly concerning the reproductive and migratory dynamics of the target species, but also differences permeated by fishers' experience and local interests. Managers initiating co-management agreements using reproduction and migration referential variables as benchmarks will be more successful if they incorporate LEK into decision-making. Regional knowledge similarities favor implementing management policies at a regional scale, potentially reducing conflicts within fishing communities and increasing resource use efficiency.

S5P16 The project "artificial nurseries", an evaluation of how these structures may modify the trophic connectivity between marinas and adjacent natural ecosystems.

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Abstract

Coastal development is one of the major threats to coastal ecosystems because it replaces natural habitats with artificial structures, thereby having important consequences for biodiversity and ecosystem services. Ecological engineering solutions such as artificial nurseries placed in highly artificial coastal habitats such as ports and marinas could contribute to the ecological rehabilitation of these systems. Even if changes in local diversity have been documented in previous studies, there is still a lack of information on how the presence of these structures could affect the export of biomass to adjacent habitats. This project aims at exploring how organic material is exported from small marinas to adjacent vegetated habitats in the Mediterranean Sea and how the presence of artificial nurseries modifies this export. We have sampled 4 marinas located on the Eastern French Mediterranean coast (PACA region) during the autumn of 2022. Two of the marinas had been equipped with specific artificial nurseries (Biohut® made by ECOCEAN company) since 2019, with the purpose of improving coastal fish recruitment. The two remaining marinas were used as control. In each site, we sampled particulate organic matter in the water column and on the surface of the sediment inside the marina (close to the mouth) and in *Posidonia oceanica* habitats situated nearby (within 300 m) and further away (c.a. 1 km). We also sampled for fishes and for their potential food sources. Samples are being processed for bulk stable isotope analyses of carbon and nitrogen and for fish stomach content. Here we will illustrate the sampling design and some preliminary results. This project contributes to a better understanding of the trophic connectivity between artificial and natural habitats and can provide valuable information on the role of ecological engineering solutions in this connectivity.